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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Cat flea hindgut a
                                                                                               Borrelia burgdorfe
                                                                                                                Human secreted pro
Bovine conglutinin
                                      Arabidopsis thalia
                                                                                                                                         Stealth virus nucl
                                                                                                                                                              Human DNA marker c
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31.2 2.2 1646 9 N82246 Rice	31.2 2.2 1551 21 C77099 H	2.2 51259 18 X83007	31.4 2.2 3463 21 C77382	31.4 2.2 1666 19 V37722	31.4 2.2 1666 16 Q95059	31.4 2.2 1627 19 V37721	31.4 2.2 1627 16 095058	31.4 2.2 1486 21 F18228	31.4 2.2 1447 20 X13590	31.4 2.2 1365 20 X85015	31.4 2.2 1333 21 649301	31.4 2.2 1330 21 036038	31.4 2.2 1299 21 A49460	31.4 2.2 1291 21 C39019	31.4 2.2 1238 21 Z52513	31.6 2.3 4473 22 F44671	31.6 2.3 2773 21 265009	31.6 2.3 2547 21 A74993	31.6 2.3 624 21 F07873	31.8 2.3 13339 19 044734	31.8 2.3 1661 19 V03875	31.8 2.3 1661 17 TASION	32 2 2423 24 752493	32 2.3 1334 21 A39409	32.4 2.3 72604 20 210752	32.6 2.3 49999 20 Z23903	32.6 2.3 9321 21 A97904 L.	32.6 2.3 7387 21 A97914 L.	32.6 2.3 6204 21 A97917	32.6 2.3 3970 21 A97911	33 2.4 1644 20 x60775	
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## ALIGNMENTS

RESULT 1 V62688

Glucuronyl C5-epimerase; cattle; D-glucuronic acid; L-iduronic acid; heparin; heparan sulphate; ss.

Bovine glucuronyl C5-epimerase cDNA.

15-FEB-1999 (first entry)

V62688;

V62688 standard; cDNA; 3085 BP

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WPI; 1998-583655/49 P-PSDB; W79263. Li J, Lindahl U; (LIJJ/) LI J. (LIND/) LINDAHL U. CDS 18-APR-1997; 17-APR-1998; WO9848006-A1. 29-OCT-1998. Bos taurus. 97SE-0001454 98WO-SE00703. Location/Qualifiers 73..1407 /\*tag= a

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catalyses the conversion of D-glucuronic acid (GlcA) to L-iduronic acid (IdoA). To isolate the sequence, highly purified epimerase acid (IdoA). To isolate the sequence, highly purified epimerase from bovine liver was subjected to digestion with a lysine-specific protease. A DNA probe was generated from bovine liver cDNA by PCR using primers (see V62689-91) based on an isolated peptide (see using primers (see V62689-91) based on an isolated peptide (see w79270). This was used to screen a bovine ling lambda 9t10 library, w79270) generate was identified and sequenced. An additional library by PCR using an epimerase-specific primer (see V62692). The invention relates to isolated or recombinant DNA sequences for the invention relates to isolated or recombinant DNA sequences for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L-iduronic acid in the synthesis of heparin and heparan sulphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transformed host cells are also claimed. The nucleic acid and vector can be used for the recombinant production of the enzyme. Glucuronyl C5-epimerase is useful for converting GlcA to IdoA in the biosynthesis of heparin and heparan sulphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a mammalian (including human) glucuronyl C5-epimerase or its amount of the functional derivative. Recombinant expression vectors and
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                        type 1 sodium transport gene; ss
                                  diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
                                                              Bovine butyrophilin;
                                                                                      Hereditary haemochromatosis subregion from an HH affected individual.
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                                                                                                                                                                                                                                                                                                                                                 agcaccattgatgagtccccaatcttcaaagaatttgtcaagaggtggaagagctacctt
                                                                                                                      (first entry)
                                                                BT; human hereditary haemochromatosis; HFE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 method to determine the presence or absence of the common hereditary
C haemochromatosis (HFE) gene mutation in an individual comprising:
C (a) providing DNA or RNA from the Individual; and (b) assessing the
C DNA or RNA for the presence or absence of a haplotype or genotype where
C the presence or absence of the haplotype or genotype where
C presence of the HFE gene mutation in the genome of the individual. The
C HFE gene sequences from the present invention can be used to develop
C products for use in the diagnosis and treatment of HFE. The present
C invention also describes BTF genes, which are homologues of the milk
C protein butyrophilin (BT), and can be used in the production of agonists
C and antagonists of BT function. Also described are: (1) a RORET gene
C which can be used to develop products for the study, diagnosis and
C treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
C which are homologues of a type 1 sodium transport gene, and can
C similarly be used for hypophosphatemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               20319 TTTTCTTTTAAATAAATTATTTAATTTGGAAGACCAAG 20282
Tandem repeat sequence; DNA isolation; intermediate tandem repeat; ITR sequence; pentanucleotide tandem repeat; stutter artifact; DNA typing; DNA profiling; linkage analysis; criminal justice; paternity testing; animal lineage analysis; microsatellite loci;
                                                                                                                      Human DNA marker clone S110.
                                                                                                                                                              23-DEC-1999 (first entry)
                                                                                                                                                                                                                 Z27743
                                                                                                                                                                                                                                                       Z27743 standard; DNA; 1366 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes hereditary haemochromatosis gene products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               haemochromatosis (HH) affected individual. Also described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 9; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-240014/21.
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01-OCT-1996;
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Pred. No. 21;
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CC This sequence represents a human DNA marker clone used in the method of CC the invention. The method is for isolating a fragment of DNA containing CC an intermediate tandem repeat (ITR) sequence using hybridization CC election, and comprises: (a) providing several DNA fragments, at least CC one of which contains an ITR sequence, a region of the DNA fragment which CC contains at least one repeat unit consisting of a sequence of five, six CC or seven bases repeated in tandem at least two times; (b) providing a stationary support having at least one oligonucleotide associated with CC it, where the oligonucleotide includes a sequence of nucleotides which is CC complementary to a portion of the ITR sequence; and (c) combining the DNA fragments with the support under conditions where the DNA fragments CC including the DNA fragment containing the ITR sequence hybridize to the Support. The method is particularly used to isolate DNA containing CC pentanucleotide tandem repeat sequences as well as to detect target ITR CC DNA sequences having a low incidence of stutter artifacts (no more than CC 2.4%). The method is useful in DNA profiling for linkage analysis. CC criminal justice, paternity testing and other forensic and medical uses. CC containing is also useful for confirming the lineage of horses, dogs and other prize animals. The invention overcomes problems related to the use of microsatellite loci in DNA profiling. The method can detect polymorphisms with a low incidence of stutter artifacts, which has more in interpretarion allelic contents of loci many the content of loci many the problem in interpretarion allelic contents to find.
Query Match
                                                                                Sequence 1366 BP; 436 A; 56 C; 594 G; 280 T; 0 other;
                                                                                                                                                                previously been a problem in interpreting allelic content of loci. The development of markers based on larger repeat units, enables easier separation of the fragments on electrophoretic gels. This allows the
                                                                                                                                                simultaneous analysis of more loci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 22; Page 86; 111pp; English
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                                                                                                                                                   1057 actacacctagctcttttgttttaaatggctttatgtattctttaattgggctgtatgac 1116
                                                                                                                                                                                                988 gagtagaacggagtgattggggtggaatggaatagagtggaatggaatggagtggagtgg 1047
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mes 92; Conserv
atggaat 1174
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"this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"  k  "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"  1  1  1  1  1  1  1  1  1  1  1  1  1	h  "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"  1  1  1  1 this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"	f "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"  g "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"	d "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"  e "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"	nucleotide is represent iffication, and is includent numbering given in the nucleotide is represent iffication, and is includent numbering given in the	Qualifiers  Qualifiers  his nucleotide is repres pecification, and is incleoting given in the second	59 BP.  Y)  Id clone, SEQ ID NO: 24.
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base numbering given in the specification"
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                                                                                                                                                                                                                                                                                     Score 35;
                                                                                                                                                                                                                                              Mismatches 164;
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nucleic acids, proteins, antibodies and (antiagonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;

parasitic infections

infectious diseases such as viral, bacterial,

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                                                                                                                                                                      the fusion protein as compared to the human protein only. The genes proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The
                                                                                                                                                                                                                                The invention relate to the isolation of genes C69084-C69119 encoding 27 human secreted proteins B37984-B38019. The genes can be used to generate fusion proteins by linking to the gene for the human immunoglobulin G Fc portion (C69075) for increasing the stability of
                                                                                                                                                                                                                                                                                                               Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; antionvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorden neurological disease; infection; human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                used as
                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecules encoding 27 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2479
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Moore PA,
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Olsen
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Sequence 2248 BP;

657 A; 460 C;

518 G;

609 T; 4 other;

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Sequence 571 BP;
 198 A;
76 C; 54 G;
 241 T; 2 other;
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Query Match

2.48;

Score 33.8;

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Best Local Similarity
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                                                       Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and
                                                                                                                                                                                                             New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                          Clayton R,
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20-JUN-1997;
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Borrelia burgdorferi (Bb). Products derived from Bb can be used for
                                                                                                                                                                                   Claim 1; Page 1109; 1128pp; English.
                                                                                                                                                                                                                                                                              WPI; 1999-081217/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection; diagnosis;
                                          endemic relapsing fever, and Lyme borreliosis, more commonly known
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                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                       22-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; Idemic relapsing fever; endemic relapsing fever; Lyme borreliosis; fection; diagnosis; characterisation; detection; ds.
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97US-0050359.
97US-0053344.
97US-0053377.
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Pred. No. 2
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Best Local Similarity
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                x20248 to x20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
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                                                                                                                                                                                                                Claim 1; Page 920-925; 1128pp; English.
                                                                                                                                                                                                                                                New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, preventle and therapy of infections, particularly Lyme disease
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Sequence 9542 BP;
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                                                                                                                                                                                                                                                                                                                                                               White OR;
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97US-0050359.
97US-0053344.
97US-0053377.
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   3812 A; 1160 C; 1113 G;
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Pred. No. 1
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constructs, recombinant varies and recombinant cells comprising the nucleic acids of the invention, recombinant production of the proteins, antibodies against the proteins, a method of identifying inhibitors of the proteins, and compositions comprising the inhibitors for cadministration to an animal. The nucleic acids, and the proteins they cancode may be used in the prevention, treatment and diagnosis of diseases cassociated with flea infestations. For example, the nucleic acids may be used to produce an HMT or HMC protein according to standard recombinant CDNA methodology by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The HMT and HMC nucleic acids may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect and quantitate the presence of cat flea or other homologous nucleic acid continuous in samples. They may also be used to study the expression and continuous proteins may be used as antigens in the production of specific antibodies, and in assays to identify modulators (agonists and massays to identify modulators (agonists and massays to identify modulators (agonists and massays to identify modulators (agonists).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cat flea; hindgut and Malpighian tubule nucleic acid; flea infestation; vaccine; antiparasitic; therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C94048 standard; cDNA; 283 BP
                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel cat flea (Ctenocephalides felis) nucleic acids which are expressed in hindgut and Malpighian tubule (HMT) tissue or head and nerve cord (HMC) tissue. The invention also relates to the encoded proteins. The invention additionally encompasses expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 26; Page 425; 964pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flea Malpighian tubule and head and nerve cord tissue derived nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0128704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; antiparasitic; therapeutic target;
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05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

29-MAR-1999

01-APR-1999

06-APR-1999

08-APR-1999
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                                                      06-MAY
06-MAY
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                                                                                                                                                                                                                                                    28-APR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana DNA fragment SEQ ID NO: 26071.
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22-0CT-11 22-0CT-11 22-0CT-11 25-0CT-12 25-0CT-12 25-0CT-12 26-0CT-12 26-0CT-11	21-0CT-1 21-0CT-1 21-0CT-1 21-0CT-1	R 21-OCT-1 R 21-OCT-1 R 21-OCT-1	R 14-0CT-1	14-0CT-1	13-0CT-1 13-0CT-1	12-OCT-1 13-OCT-1	07-0CT-1	05-0CT-1	29-SEP-1	24-SEP-1	20-SEP-1 22-SEP-1	15-SEP-1				AUG-1	R 26-AUG-1 R 27-AUG-1	R 23-AUG-1 R 25-AUG-1	R 20-AUG-1999	R 20-AUG-1999 R 20-AUG-1999	R 18-AUG-1999	R 16-AUG-1999	R 13-AUG-1999	99	10-AUG-1999	09-AUG-1999	06-AUG-1	05-AUG-1	04-AUG-1	02-AUG-1	02-AUG-1
22-OCT-1999; 22-OCT-1999; 25-OCT-1999; 25-OCT-1999; 25-OCT-1999; 26-OCT-1999; 26-OCT-1999;	21-OCT-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999;	R 18-OCT-1999; R 21-OCT-1999; R 21-OCT-1999;	R 14-OCT-1999; R 14-OCT-1999;	14-0CT-1999; 14-0CT-1999; 14-0CT-1999;	13-OCT-1999; 13-OCT-1999;	12-OCT-1999; 13-OCT-1999;	07-0CT-1999;	05-OCT-1999; 06-OCT-1999;	29-SEP-1999;	24-SEP-1999;	20-SEP-1999; 22-SEP-1999; 23-SEP-1999;	15-SEP-1999; 16-SEP-1999;	1999; 1999;	1999;	. 6661 . 6661	AUG-1999;	R 26-AUG-1999; R 27-AUG-1999;	R 23-AUG-1999; R 25-AUG-1999;	R 20-AUG-1999; R 23-AUG-1999;	R 20-AUG-1999;	R 18-AUG-1999;	R 16-AUG-1999;	R 13-AUG-1999;	-1999; -1999;	10-AUG-1999;	09-AUG-1999;	06-AUG-1999;	05-AUG-1999;	04-AUG-1999; 04-AUG-1999;	02-AUG-1999; 03-AUG-1999;	02-AUG-1999; 02-AUG-1999;
22-OCT-1999; 99US-016 22-OCT-1999; 99US-016 25-OCT-1999; 99US-016 25-OCT-1999; 99US-016 25-OCT-1999; 99US-016 25-OCT-1999; 99US-016 26-OCT-1999; 99US-016	21-OCT-1999; 99US-016 21-OCT-1999; 99US-016 21-OCT-1999; 99US-016 21-OCT-1999; 99US-016	R 18-OCT-1999; 99US-01: R 21-OCT-1999; 99US-01: R 21-OCT-1999; 99US-01:	R 14-OCT-1999; 99US-01; R 14-OCT-1999; 99US-01;	14-OCT-1999; 99US-01: 14-OCT-1999; 99US-01: 14-OCT-1999; 99US-01:	13-OCT-1999; 99US-01: 13-OCT-1999; 99US-01:	12-OCT-1999; 99US-01:	07-0CT-1999; 99US-01:	05-OCT-1999; 99US-01: 05-OCT-1999; 99US-01:	28-SEP-1999; 990S-01 29-SEP-1999; 990S-01	24-SEP-1999; 99US-01:	20-SEP-1999; 99US-01 22-SEP-1999; 99US-01 23-SEP-1999; 99US-01	15-SEP-1999; 99US-01	1999; 99US-01 1999; 99US-01	1999; 99US-01 1999; 99US-01	1999; 99US-01 1999: 99US-01	AUG-1999; 99US-01	R 26-AUG-1999; 99US-01 R 27-AUG-1999; 99US-01	R 23-AUG-1999; 99US-01 R 25-AUG-1999; 99US-01	R 20-AUG-1999; 99US-01 R 23-AUG-1999; 99US-01	R 20-AUG-1999; 99US-01	R 18-AUG-1999; 99US-01	R 16-AUG-1999; 99US-01	R 13-AUG-1999; 99US-01 R 13-AUG-1999; 99US-01	-1999; 99US-01 -1999; 99US-01	10-AUG-1999; 99US-01	09-AUG-1999; 99US-01	06-AUG-1999; 99US-01	05-AUG-1999; 99US-01	04-AUG-1999; 99US-01 04-AUG-1999; 99US-01	02-AUG-1999; 99US-01	02-AUG-1999; 99US-01 02-AUG-1999; 99US-01
22-OCT-1999; 22-OCT-1999; 25-OCT-1999; 25-OCT-1999; 25-OCT-1999; 26-OCT-1999; 26-OCT-1999;	21-OCT-1999; 99US-016 21-OCT-1999; 99US-016 21-OCT-1999; 99US-016 21-OCT-1999; 99US-016	R 18-OCT-1999; 99US-015 R 21-OCT-1999; 99US-016 R 21-OCT-1999; 99US-016	R 14-OCT-1999; 99US-015 R 14-OCT-1999; 99US-015	14-0CT-1999; 99US-015 14-0CT-1999; 99US-015 14-0CT-1999; 99US-015	13-OCT-1999; 99US-015 13-OCT-1999; 99US-015	12-OCT-1999; 99US-015	07-OCT-1999; 99US-015	05-0CT-1999; 99US-015 05-0CT-1999; 99US-015	28-SEP-1999; 990S-015 29-SEP-1999; 990S-015	24-SEP-1999; 99US-015	20-SEP-1999; 99US-015 22-SEP-1999; 99US-015	15-SEP-1999; 99US-015	1999; 99US-015 1999; 99US-015	1999; 99US-015	1999; 99US-015 1999; 99US-015	AUG-1999; 99US-015	R 26-AUG-1999; 99US-015 R 27-AUG-1999; 99US-015	R 23-AUG-1999; 99US-014 R 25-AUG-1999; 99US-015	R 20-AUG-1999; 99US-0149929 R 23-AUG-1999; 99US-0149902	R 20-AUG-1999; 99US-014	R 18-AUG-1999; 99US-014	R 16-AUG-1999; 99US-014	R 13-AUG-1999; 99US-014 R 13-AUG-1999; 99US-014	-1999; 99US-014 -1999; 99US-014	10-AUG-1999; 99US-0148171	09-AUG-1999; 99US-0147493	06-AUG-1999; 99US-0147303	05-AUG-1999; 99US-0147192 05-AUG-1999; 99US-0147260	04-AUG-1999; 99US-014-014-014-014-014-014-014-014-014-014	02-AUG-1999; 99US-0146389 03-AUG-1999; 99US-0147038	02-AUG-1999; 99US-01:
22-OCT-1999; 99US-016; 22-OCT-1999; 99US-016; 25-OCT-1999; 99US-016; 25-OCT-1999; 99US-016; 25-OCT-1999; 99US-016; 26-OCT-1999; 99US-016; 26-OCT-1999; 99US-016;	21-OCT-1999; 99US-016 21-OCT-1999; 99US-016 21-OCT-1999; 99US-016 21-OCT-1999; 99US-016	R 18-OCT-1999; 99US-015 R 21-OCT-1999; 99US-016 R 21-OCT-1999; 99US-016	R 14-OCT-1999; 99US-015 R 14-OCT-1999; 99US-015	14-0CT-1999; 99US-015 14-0CT-1999; 99US-015 14-0CT-1999; 99US-015	13-OCT-1999; 99US-015 13-OCT-1999; 99US-015	12-OCT-1999; 99US-015	07-OCT-1999; 99US-015	05-0CT-1999; 99US-015 05-0CT-1999; 99US-015	28-SEP-1999; 990S-015 29-SEP-1999; 990S-015	24-SEP-1999; 99US-015	20-SEP-1999; 99US-015 22-SEP-1999; 99US-015	15-SEP-1999; 99US-015	1999; 99US-015 1999; 99US-015	1999; 99US-015	1999; 99US-015 1999; 99US-015	AUG-1999; 99US-015	R 26-AUG-1999; 99US-015 R 27-AUG-1999; 99US-015	R 23-AUG-1999; 99US-014 R 25-AUG-1999; 99US-015	R 20-AUG-1999; 99US-0149929 R 23-AUG-1999; 99US-0149902	R 20-AUG-1999; 99US-0149722 R 20-AUG-1999; 99US-0149723	R 18-AUG-1999; 99US-014	R 16-AUG-1999; 99US-014	R 13-AUG-1999; 99US-014 R 13-AUG-1999; 99US-014	-1999; 99US-014 -1999; 99US-014	10-AUG-1999; 99US-0148171	09-AUG-1999; 99US-0147493	06-AUG-1999; 99US-0147303	05-AUG-1999; 99US-0147192 05-AUG-1999; 99US-0147260	04-AUG-1999; 99US-0147204 04-AUG-1999; 99US-0147302	02-AUG-1999; 99US-0146389 03-AUG-1999; 99US-0147038	02-AUG-1999; 99US-01:

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Query Match
Best Local :
                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V44080/c
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                                                                                   construction of a novel expression vector. This vector contains a gene recombination having a strong expression-inducing promoter in the plasmid and induces high productivity of recombinant protein in a productivity transformant of a protein which is a G418 resistant cell recombined with a protein gene. This expression vector can produce high productivity transformant of a protein which is a G418 resistant cell recombined with a protein gene. This expression vector can produce high levels of the recombinant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                 Sequence 1392 BP; 348 A; 370 C; 426 G; 248 T; 0 other;
                                                                                                                                                                                                         V44053-V44087 are DNA sequences used in a method resulting in the
                                                                                                                                                                                                                                        Disclosure; Page 25-26; 35pp; Japanese.
                                                                                                                                                                                                                                                              gene cistron and multi-cloning site for gene recombination
                                                                                                                                                                                                                                                                        Expression vector for mammalian cell - comprises phosphotransferase
                                                                                                                                                                                                                                                                                                              WPI; 1998-430954/37.
                                                                                                                                                                                                                                                                                                                                                                   23-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DHFR; NEO-r; expression vector; neomycin phosphotransferase gene;
expression-inducing promoter; G418-resistant cell; ds.
                                                                                                                                                                                                                                                                                                                                       (IMMO ) IMMUNO JAPAN INC.
                                                                                                                                                                                                                                                                                                                                                                                            25-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                              JP10179169-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mu-NEO-r DNA fragment #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V44080;
                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V44080 standard; cDNA; 1392 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1151 aagcgaggtccttgtatgagcgtggcatggaa 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1031 aacatgactggtatgaagaatatccaactacacctagctcttttgttttaaatggcttta 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1091 tgtattctttaattgggctgtatgacttaaaagaaactgcaggggaaaactcgggaaag 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      574 aacagaggtcatgatatcatgttgaaattcaa 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    514 gttagtaataaatttggattgcttcgtagccagtatctgccttctaataccaccattaag 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      454 aaaatgtgtggaataggcaaaatgcaatctcctattgatcttcgggacaaaaatgtggta 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-OCT-1999;
28-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                66;
                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      97JP-0243357.
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99US-0161920.
99US-0161992.
99US-0161993.
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                    2.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.4%;
           0;
                   Score 33.6; D
Pred. No. 3.8;

 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33.6; DB 21; Length 1231; Pred. No. 3.5;
      Mismatches
                           DB 19; Length 1392;
      54;
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     Indels
    0;
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 Gaps
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0;
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FH XX
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                                  The nucleic acid is used in the production of bovine conglutinin, either the complete protein, or amino acid regions 1-351, 197-351 or 250-351. Oligomers based on the nucleic acid are used to modulate response. They are also useful as primers and probes for therapeutic or diagnostic use. Conglutinin, or its carbohydrate-binding fragments, are used to bind cells carrying the Clq receptor. Solid supports are used to remove compounds (especially proteins or peptides, e.g. immune complexes) having a carbohydrate component able of hound compounds.
Sequence 1534 BP; 395 A; 398 C; 458 G; 283 T; 0 other;
                                                                                                                                                                                                                Claim 1; Fig 1A-1B; 29pp; English.
                                                                                                                                                                                                                                                    New nucleic acid encoding bovine conglutinin and its fragments - and related vectors, host cell, etc. useful e.g. in modulating conglutinin expression or for selective removal of cpds., carrying
                                                                                                                                                                                                                                               particular carbohydrate residues.
                                                                                                                                                                                                                                                                                                                               P-PSDB; R75642.
                                                                                                                                                                                                                                                                                                                                                                   Lee YM, Leiby KR, Okarma TB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                           (UYBO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMU-) APPLIED IMMUNE SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conglutinin; therapeutic; diagnostic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine conglutinin nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q92554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q92554 standard; cDNA; 1534 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1235 acctocygcacttcatgcttggcattgcccccaacctggcccgctgggactatcacacca 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1175 gcatggaatcccttaaagccatgctccccttgtacgacactggctcaggaaccatctatg 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            704 TCCCCCTTCAGTCCTGGGGGGCCCCTGGCACCTGAAGGGCCCTGTGGACCTATTGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       764 GCATTGACCTCTGCAAGCCCACTCTCCCCCTTTGCTCCTGTTTCTCCAAGGATCACCTCTG 705
                                                                                                                                                                                                                                                                                                                                          1995-231510/30.
                                                                                                                                                                                                                                                                                                                                                                                                        UNIV BOSTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-0168458.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= 1
231..290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "bovine 291..1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
231..1346
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                                                                                                                                                                                                                                                                                                                                                                   Sastry K;
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Matches Best Local

66;

Conservative

0

Similarity

2.4%;

Score 33.6; Pred. No. 4. Mismatches

DB 16; 54;

Length 1534; Indels

0 Gaps

0;

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RESULT 12
X60775/c
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1235 acctccggcacttcatgcttggcattgcccccaacctggcccgctgggactatcacacca 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    x60775 standard; cDNA; 1644 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soybean; Solanaceae crop plant; cytochrome p450; transgenic plant; enzyme; phenylurea herbicide; herbicide resistance; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soybean cytochrome P450 enzyme, CYP77A3 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      x60775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       829 TCCCCCTTCAGTCCTGGGGGGCCCCTGGCACCTGAAGGGCCCTGTGGACCTATGGCTCCA 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            889 GCATTGACCTCTGCAAGCCCACTCTCCCCCCTTTGCTCCTGTTTCTCCAGGATCACCTCTG 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9919493-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                    The invention provides new DNA molecules (X60773-X60781) encoding soybean cytochrome P450 enzymes (Y09183-Y09191) respectively. The DNA encoding the cytochrome P450 enzymes is useful for transformation of Solanaceae the cytochrome P450 enzymes is useful for transformation of Solanaceae crop plants. Transgenic plants comprising DNA constructs having the P450 crop provided acid sequences are resistant to phenylurea herbicides. The transgenic plants have increased resistance to phenylurea herbicides compared to wild-type plants of the same species. The plant crops, e-9. turifyrass, tobacco, potato, tomato, corn, rice, cotton, soybean, rape, wheat, oats, barley or rice are particularly resistant to fluometuron, linuren.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYNC-) UNIV NORTH CAROLINA STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 48-51; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding soybean cytochrome P450 enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; Y09185
                                                                                                                                                                                                                           Sequence 1644 BP; 482 A; 366 C; 400 G; 396 T; 0 other;
                                                                                                                                                                                                                                                             linuron, chlortoluron or diuron
696 AATTGGAAGATAGTCATCAATTCTCGGGTCCAAAGTGATGAGAACACTCTTCA 644
                              459 aaatggaagcgtgtctgtggttctggagacgacagaaaagaatcagctcttca 511
                                                                   756 AACCTGTTCTCTGCGAACCTCCAAGGCTTTCTTTCTTTGCTTTGAGAAAAAGGGGCTTAG 697
                                                                                                 399 atccttgcaactggggaacacaaaagattttattatttcatttgacctcaagttcttaac 458
                                                                                                                                        Local Similarity
les 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-302532/25.
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0948564.
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                                                                                                                                                           2.4%; Score 33; DB 55.8%; Pred. No. 6.5;
                                                                                                                                                0;
                                                                                                                                                  Mismatches
                                                                                                                                                                                  DB 20; Length 1644;
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RESULT

13

A97917 standard; DNA; 6204 BP.

A97911

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X PD X PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel nucleic acid molecule (I) encoding an CC alternan sucrase (E.C. 2.4.1.140 - an enzyme, that belongs to the CR alternan sucrase (E.C. 2.4.1.140 - an enzyme, that belongs to the CR carbohydrates group) The recombinant, purified alternan sucrase CR gene is useful for the fermentative production of alternan (a CR carbohydrate) and/or fructose by secreting the enzyme into a CR carbohydrate) and/or fructose by secreting the enzyme into a CR contacted with a saccharose-containing solution. The alternan and/or CR criticise is then isolated from the medium. Cosmetic products or CR foodstuffs containing alternan can be produced. Recombinant production of foodstuffs containing alternan can be produced. Recombinant production of alternan sucrase is advantageous as it provides a cost effective means of a producing fructose for high fructose containing syrups, production of CR producing fructose for high fructose containing syrups, production of CR cathoh previously has been achieved by costly production from maize CR which previously has been achieved by costly production from maize can be protein isolated from clone AS-19B2 which is described in the
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L. mesenteroides alternan sucrase DNA from clone AS-19B2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 41-43; 64pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding recombinant Leuconostoc mesenteroides
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3970 BP; 1354 A; 651 C; 823 G; 1142 T; 0 other;
                                                                                                                                                                                                                    1605 tgttggtaataaccctgaccttaagttgaacaatgataagaccattaccttgcatatggg 1664
                                                                                                                                                                                                                                                                                                                                                                                                                                              method of the invention.
                                                          1725 tgtttatgatagtga 1739
                                                                                                                                      1665 aaaggogcataagaatcaactttacogtgoottagtattatcaaatgactcaggaattga 1724
                                                                                                 546 ttttaaagaaagaga 560
                                                                                                                                                             486 gacgacagaaaagaatcagctcttcactgtacattatgtctcaaatacccagctaattgc 545
                                                                                                                                                                                                                                                          426 ttttattatttcatttgacctcaagttcttaacaaatggaagcgtgtctgtggttctgga 485
                                                                                                                                                                                                                                                                                                                     Match 2.3%;
Local Similarity 52.6%;
                                                                                                                                                                                                                                                                                                          71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Welsh T,
                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                              Score 32.6; DB 21; Length 3970; Pred. No. 15;
                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Knuth K;
                                                                                                                                                                                                                                                                                                                   64; Indels
                                                                                                                                                                                                                                                                                                                       0;
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RESULT 15
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A97914 standard; DNA; 7387 BP.
                                                                                            2907 tgtttatgatagtga 2921
                                                                                                                                         2847 aaaggegeataagaateaaetttaeegtgeettagtattateaaatgaeteaggaattga 2906
                                                                                                                                                                                                                 2787 tgttggtaataaccctgaccttaagttgaacaatgataagaccattaccttgcatatggg 2846
                                                                                                                             546 ttttaaagaaagaga 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucosyltransferase group) The recombinant, purified alternan sucrase gene is useful for the fermentative production of alternan (a carbohydrate) and/or fructose by secreting the enzyme into a contacted with a saccharose containing solution. Alternatively, the enzyme is fructose is then isolated from the medium. Cosmetic products or alternan sucrase is then isolated from the medium. Cosmetic products or alternan sucrase is advantageous as it provides. Recombinant production of producing fructose for high fructose containing syrups, production of which previously has been achieved by costly production from maize starch. This sequence represents a Leuconostoc mesenteroides alternan sucrase in analysis a Leuconostoc mesenteroides alternan sucrase in production from maize starch.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6204 BP; 2101 A; 1038 C; 1354 G; 1711 T; 0 other;
                                                                                                                                                                                486 gacgacagaaaagaatcagctcttcactgtacattatgtctcaaatacccagctaattgc 545
                                                                                                                                                                                                                                            426 ttttattatttcatttgacctcaagttcttaacaaatggaagcgtgtctgtggttctgga 485
                                                                                                                                                                                                                                                                                                                                                                                                                                             sucrase protein encoding DNA insertion sequence which is described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel nucleic acid molecule (I) encoding an alternan sucrase (E.C. 2.4.1.140 - an enzyme, that belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding recombinant Leuconostoc mesenteroides alternan sucrase protein and methods of alternan and fructose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-550294/51
                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kossmann J,
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(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
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                                                                                                                                                                                                                                                                                                                                2.3%; Score 32.6;
52.6%; Pred. No. 20;
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Search completed: May 25, 2001, 03:59:24 Job time: 3280 sec

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3578 tgtttatgatagtga 3592
                                        3518 aaaggogoataagaatoaactttaoogtgoottagtattatoaaatgaotoaggaattga 3577
                                                                                                    3458 tgttggtaataaccctgaccttaagttgaacaatgataagaccattaccttgcatatggg 3517
                    546 ttttaaagaaagaga 560
|  |  |  |  |  |  |  |  |
                                                                                                                                                                                                                                                                                     carbohydrate) and/or fructose by secreting the enzyme into a contacted with a saccharose-containing culture medium. Alternatively, the enzyme is fructose is then isolated from the medium. Cosmetic products or alternan sucrase is advantageous as it provides a cost effective means of producing fructose for high fructose containing syrups, production of which previously has been achieved by costly production from maize sucrase 3'-UTR DNA fragment which is described in the method of
                                                                                                                                                                                                                                                  Sequence 7387 BP; 2469 A; 1218 C; 1581 G; 2119 T; 0 other;
                                                           486 gacgacagaaaagaatcagctcttcactgtacattatgtctcaaatacccagctaattgc 545
                                                                                                                       426 tittattatticatitgacotcaagticttaacaaatggaagcgigictgiggitcigga 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel nucleic acid molecule (I) encoding an alternan sucrase (E.C. 2.4.1.140 - an enzyme, that belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 46-50; 64pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding recombinant Leuconostoc mesenteroides alternan sucrase protein and methods of alternan and fructose
                                                                                                                                                                                                                Local
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(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
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Similarity 52.6%;
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Pred. No. 22;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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FOWLPOX VIRUS lite 500  0, Version #1 463 313 300.6	57-073 52-725 58-856 68-856 68-859 11-9420 11-9420 13-336 13-336 13-752 18-983 13-983 10-983 10-983 10-983 10-983 10-983 10-983 10-983 10-983 10-983 10-983 10-983 10-983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
NUMBER OF SEQUENCES: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 cagattgcacagtatgggttaagtcactacagcaagaatctaactgaaaaacccccctcat 246,
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Local Similarity 6.2%; Pred. No. 0.13;
hes 26; Conservative 207; Mismatches 188; Indels 0
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                                                                                                                                      CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                            STREET: 3174 POI
CITY: PALO ALTO
                                                                                                                                                                                                                                                             COUNTRY:
                CLASSIFICATION:
                                                                                    CLASSIFICATION:
                                                                                                      FILING DATE:
                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                             94304
                                                                                                                                                                                                                                                                                CALIFORNIA
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Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bandman, Olga
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                                                                                                                                                                                                                                                                                                                                 INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                          Floppy disk
                                  March 27, 1998
                                                                                                      Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                      Karl J
                                                        60/079,677
                                                                                                                         US/09/276,531
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US-09-276-531-29
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Best Local Similarity 48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08948564 Patent No. 6121512 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (650) 845-41
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Corbin, Frederick T.
TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 tgataagtcaagattcaccaatgttaaacagttcattgctccagaaaccagtgaaggtgt 398
                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                     REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 50:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 010
                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,09
                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 ATATCAAGAAGTATGTCTTGTCCTTTTGGCCAAAGAAAAAGTGAAGCCGTTAACTTAGC 180
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                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: 919-854-1401
                                                                                                                             CLASSIFICATION:
                                                                                                                                             FILING DATE:
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                   TELEPHONE:
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Dewey, Ralph E.
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INFORMATION FOR SEQ ID NO:

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Patent No. 555231
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APPLICANT: Lim, Bing
APPLICANT: Adra, Chaker N.
                                                                                                                                                    TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1661 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,
                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                             FEATURE:
                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: RECOMBINANT HTM4 GENE, PROTEIN AND
TITLE OF INVENTION: ASSAYS
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             NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
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        CDS
97..741
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US-08-707-340-3
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          Matches
                      Query Match
Best Local Similarity
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Best Local Similarity 56.1%;
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                                                                                                                                                                                                                                    TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 861-6240
                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 06-OCT-PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lim, Bing
APPLICANT: Adra, Chaker N.
APPLICANT: Lelias, Jean-Michel
TITLE OF INVENTION: RECOMBINANT HTM4 GENE, PROTEIN AND
TITLE OF INVENTION: ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1292 AACCCTCCCATCTCAAATACAGTGAAAATTTATTTTAATGATAATGA 1246
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                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                              NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 03-JUL-1996
                                                                                                      LOCATION:
                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: BIH94-03A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 03-SEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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        Conservative
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97..738
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                                                                                                                                                   DNA (genomic)
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                                                                                                                                                                                    single
                      2.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 08/318,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/707,340
   Score 31.8; DB 1; Length 1661; Pred. No. 3.4; 0; Mismatches 47; Indels 0
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   0;
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Gaps
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1292 AACCCTCCCATCTCAAATACAGTGAAAATTTATTTTAATGATAATGA 1246

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US-08-994-578-3/c
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US-08-994-578-3
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                                                                                                                                              Matches
                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 03-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/318
FILING DATE: 06-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: BEOOK, DAVID E.
REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3:
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APPLICANT: Adra, Chaker N.
APPLICANT: Lelias, Jean-Michel
TITLE OF INVENTION: HTM4 METHO
TITLE OF INVENTION: AGONISTS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1661 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: BI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/675,648
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                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                    1352 TTTACATATCAGGGCATGTGTGAGTTCCAGCAGTTCACTGAAATAAAATCCCCTGAGCCTT 1293
1292 AACCCTCCCATCTCAAATACAGTGAAAATTTATTTTAATGATAATGA 1246
                              454 ttaacaaatggaagcgtgtctgtggttctggagacgacagaaaagaatcagctcttcact 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US OF STITLING DATE: 03-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/994,578 FILING DATE: December 19, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                           Local Similarity 56.18;
tes 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                              Score 31.8; DI Pred. No. 3.4; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIH94-03A2Z
                                                                                                                                                                                   DB 2;
                                                                                                                                                  47;
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                                                                                                                                                  Indels
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US-08-615-170-2
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                                                                                                                                                                                 Matches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: PCT/US95/01526
FILING DATE: 06-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                        1119 ATGGTGTTTCCAGTCAATATGAGAGCCCAGAAAATATGGTCATTACCTGTTCCACTAAAG 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1627 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                     1179 TGTGTTCCTTTGGAAAGCAGGTGGTGGAGAAAGTGGAGACAGAGTATGCACACTATGAAA 1238
                                                                                                                                                                                                                                                                                                                                               FEATURE:
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452 tettaacaaatggaagegtgtetgtggttetggagaegaeagaaaagaatcagetettea 511
                                                                                                                               392 aaggtgtatcottggcaactggggaacacaaaagattttatttatttcatttgacotcaagt 451
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STATE: California
                                                                                                                                                                        y match 2.2%;
Local Similarity 48.6%;
hes 86; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Heslin, James M. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /product= "TEF-1A"
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STEWART, Alexandre F.R. LARKIN, Sarah B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAR, Janet H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZAKIE, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HALL, Deborah E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FARRANCE, Iain K.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (415) 326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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 Mismatches

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; LCCATION: 536..571
; OTHER INFORMATION: /product= "KTQVDKYDFSSEK"
US-08-615-170-4
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                                                                     Matches
                                                                                       Best
                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29.54
REFERENCE/DOCKET NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                         NFORMATION FOR SEQ ID NO:
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392 aaggtgtatccttgcaactggggaacacaaaagattttattatttcatttgacctcaagt 451
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1666 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1239 ATGGACACTATGCCTATCGCATTCATCGTTCTCCTCTGTGAATACATGATAAACT 1295
                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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APPLICATION NUMBER: US 0:
FILING DATE: 04-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01526
FILING DATE: 06-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: STEWART, Alexand APPLICANT: LARKIN, Sarah B. TITLE OF INVENTION: DTEF-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentTn political
                                                                                    Local Similarity
                                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 185.
                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                        /product= "TEF-1B"
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                                                             0; Mismatches
                                                                          Score 31.4; DB 1; Length 1666; Pred. No. 4.6;
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                                                          91; Indels
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Sequence 209, Appr
No. 6090620
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 209:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
9117 AACCTCCAGAACTCCAAATAGACTGGACAAGAA 9149
                                                               9057 CAAAATTATAGAAGAAAACTTCCATAACCTAAAGAAAGCGATGTCCATGAACATACAAGA 9116
                                                                                                                                   8997 GATAATAGGTATAGAAGAAAGTGAAGATTCCCCAACTCAAAGGGGCCAGTAAATATCTTCAA 9056
                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                              657 agctgtcaagccaacaagaataatgcccaagaa 689
                                                                                             597 cacagttacccgggacctggtcactgacctcaggaaaggagtgggtctttccaacacaaa 656
                                                                                                                                                        537 gctaattgcttttaaagaaagagacatatactatggcatcgggcccagaacatcatggag 596
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1278 ATGGACACTATGCCTATCGCATTCATCGTTCTCCTCTGTGAATACATGATAAACT 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1218 TGTGTTCCTTTGGAAAGCAGGTGGTGGAGAAAGTGGAGACAGAGTATGCACACTATGAAA 1277
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wes 77; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                               linear
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                                                                                 Sequence 4, Application US/08147812 Patent No. 5766909
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                   GENERAL
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OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CARL SAVERIO FALCO
APPLICANT: DOMINICK ANTHONY GUIDA, JR.
APPLICANT: MARY ELIZABETH HARNETT LOCKE
              APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
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ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                                                                       3320 TTTATGTCACAGACTCACAGGCCAGGCTACC 3350
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                                                                    INFORMATION:
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Calaycay, Jimmy Ramos
                  Xie, Qiao-wen
Nathan, Carl F.
Mumford, Richard A.
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Pred. No. 10;
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COUNTRI
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
MEDIUM TYPE: Macintosh Centris650
ACCUMENT MACINTOSH 7.0.
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                                                                                      CURRENT APPLICATION NUMBER: US/09/123,708
CURRENT FILING DATE: 1998-07-28
EARLIER APPLICATION NUMBER: 08/553,503
                                                                                                                                              TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS FILE REFERENCE: 511169-2003
                                                                                                                                                                                                       APPLICANT: SCHRADER, Juergen APPLICANT: GOEDECKE, Axel
                 EARLIER FILING DATE: 1996-03-01
EARLIER APPLICATION NUMBER: P4411402.8
EARLIER FILING DATE: 1994-03-31
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEPAX: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 02-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/841,641
FILING DATE: 02-FEB-1992
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LENGTH: 4041 bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                            2106 CACAGCATACCTGAAGGTGTGAGTTCTCTAAGCATGAACAGAGATTTCTTCAGAGT 2047
                                                                                                                                                                                                                                                                                                                                                                        2046 CTGCCCATTGCTGGGACAGTCTCCAT 2021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid STRANDEDNESS: sing
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Pred. No. 13
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US-08-147-812-6/c
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                                                               Sequence 6, Application US/08147812
Patent No. 5766909
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; ORGANISM: Cytomegalovirus
US-09-123-708-1
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 74; Conserv
                   GENERAL INFORMATION:
APPLICANT: Xie, Qiao-wen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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SEQ ID NO 1
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Patent No. 6149936
GENERAL INFORMATION:
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APPLICANT: GODECKE, AXEL
TITLE OF INVENTION: DAM EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
FILE REFERENCE: 511169-2004
CURRENT APPLICATION NUMBER: US/09/123,624
CURRENT FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 08/553,503
PRIOR APPLICATION NUMBER: 08/553,503
PRIOR PILING DATE: 1996-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1994-03-3
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.2%; Score 30.8; Best Local Similarity 50.7%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1
LENGTH: 4110
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                                                                                                                                                                                 1982 CTGCCCATTGCTGGGACAGTCTCCAT 1957
APPLICANT: Nathan, Carl F.
                                                                                                                                                                                                                                                                                                                                   2102 CTGGTCGATGTCATGAGCAAAGGCGCAGAACTGAGGGTACATGCTGGAGGCCAAGGCCAAA 2043
                                                                                                                                                                                                                                                       2042 CACAGCATACCTGAAGGTGTGGTTGAGTTCTCTAAGCATGAACAGAGATTTCTTCAGAGT 1983
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; Sequence 1, Application US/08701582D
; Patent No. 6017755
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US-08-701-582D-1
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Matches 74; Conservative
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                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Floopy Disk
COMPUTER: Macintosh Centris650
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,812
FILING DATE: No. 5766000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                         APPLICANT: WRANA, Jettrey
APPLICANT: ATTISANO, Liliana
APPLICANT: SCHERER, Stephen W.
TITLE OF INVENTION: MADR2 TUMOUR SUPPRESSOR GENE
                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 2106 CACAGCATACCTGAAGGTGTGGTTGAGTTCTCTAAGCATGAACAGAGATTTCTTCAGAGT 2047
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REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W III
                                                                                                                                                                                                                                                                                                                                                                                                        673 agaataatgcccaagaaggtggttaggttgattgcgaaaggggaagggcttccttgacaac 732
             CITY: Alexandria
STATE: Virginia
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   COUNTRY:
                                                   STREET:
                                                                  ADDRESSEE:
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APPLICANT: Calaycay, Jimmy Ramos
TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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P.O. Box 1404
U.S.A.
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126 East Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : (908) 594-3905
(908) 594-4720
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                                                             Doane, Swecker & Mathis
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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER TEADABLE FORM:

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/701,582D
FILING DATE: 2-RUG-1996
CLASSIFICATION UNMBER: 030,427
REPERENCE/DOCKET NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 30,429
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 30,429
REGISTRATION NUMBER: 30,429
REGISTRATION
REGISTR
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Sequence:

Run on:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gb\_est48:\*
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gb\_est54:\*
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gb\_est56:\*
gb\_est58:\*

gb\_est78:\*
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gb\_est81:\*

gb\_est84:\* gb\_est85:\* gb\_est82:\*
gb\_est83:\* gb\_est65:\*
gb\_est66:\*

gb\_est64:\* gb\_est63:\* gb\_est62:\* gb\_est60:\* gb\_est59:\*

gb\_est76:\*
gb\_est77:\*

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Result
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                                                                                                                                                                                                    pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
Score
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21 AI521253
114 AW383386
7 AA435342
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1100
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107
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         0 BE861166
0 BB579985
0 BB579985
0 AV672171
7 AW605325
0 AV676110
                                                   AI467374
AI467374
3 BE170776
3 BF080558
4 AI981391
                                                                                                                                        A1860635
AU139373
   CNS02E30
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gb\_est90:\*
gb\_est99:\*
gb\_est100:\*
gb\_est101:\*
gb\_est103:\*

gb\_est89: gb\_est88:\* gb\_est87:\* gb\_est86:\*

gb\_est106:\*
gb\_est67:\*
gb\_est68:\*
gb\_est69:\*

gb\_est104:\* gb\_est105:\*

gb\_est72:\* gb\_est73:\*

gb\_est71:\*

gb\_est74:\*
gb\_est91:\*

gb\_est92:\*
gb\_est94:\*
gb\_est95:\*
gb\_est95:\*
gb\_est97:\*
gb\_est97:\*
gb\_est97:\*
gb\_est97:\*
em\_gss\_hum1:\*
em\_gss\_hum2:\*

em\_gss\_hum5:\*
em\_gss\_hum6:\* em\_gss\_hum3:\* em\_gss\_hum4:\*

A1860635 w104a09.x
A0139373 A0139373
AW383385 PM3-HT034
A1521253 tco66h09.x
AW383386 PM3-HT034
AA35342 vd49909.s
AA794925 vr48904.s
AL170467 Tetraodon
A1467374 vd49909.x
BEE170776 0V4-HT053
BEF080558 231598 MA
A1981391 pat.pk005
BE8611166 UI-M-AM0-BE57985 BB579985
AV672171 AV672171
AW605325 QV3-DT004
AV675110 AV676110
AL193221 Tetraodon

Description

em\_gss\_inv1:\* em\_gss\_inv2:\* em\_gss\_hum9:\*

em\_gss\_other: \* em\_gss\_inv3:\*

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FEATURES
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                                                                                                                                             Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 950

Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
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h quality sequence stop: 420.
                                                                                                                                                                                                                                                                                   Robert_Strausberg@nih.gov
/db_xref="taxon:9606"
/clone="IMAGE:2423896"
/clone_lip="NCI_CGAP_UTI"
/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH108"
                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
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Contact: Tak
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
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Similarity 92.7%;
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/note="Vector: pME18SFL3"
151 c 177 g 197
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/clone_lib="PLACE1"
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                                                                                                                                                                                          243 tcatatagaggtatatgaaacagcagaagacagggacaaaaacagccaagcccaatgactg
363 taaacagttcattgctccagaaaccagtgaaggtgtatccttgcaactggggaacacaaa 422
                                                            303 gactgtgcccaagggctgctttatggctagtgtggctgataagtcaagattcaccaatgt 362
                                                                                                               68 TCACATAGAGGTATATGAAACAGCAGAAGACAGAGACAAAAA---CAAGCCTAATGACTG
                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW383385 653 bp mRNA EST 04-FEB-2000 pM3-HT0347-091199-001-b06 HT0347 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                           572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW383385.1 GI:6888044
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Seq primer: puc 18 forward
High quality sequence start: 38
High quality sequence stop: 567.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM36t2=PM3-HT0347-
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                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) Profiles into the pUC 18 vector. Reverse transcription of profiles into the puc 18 vector.
                                                                                                                                                                                                                                                                                                                                                                                         tissue mRNA and cDNA amplification were performed under low stringency conditions."
131 c 143 g 164 t
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/clone_lib="HT0347"
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92.18;
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                                                                                                                                                                                                                                                                                                Score 521; DB 114;
Pred. No. 2.9e-143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425 TACCAGGGACCTGGTCACTGACCTCAGGAAAGGAGTGGGTCTTTCAAACACAAAAGCTGT
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                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
WWW-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1602 Std Error: 0.00
Seg primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
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                                                                                                                                                                                    quality sequence stop: 376
                                                                                                                                                                                                                                                                                                                                                                                                   Robert_Strausberg@nih.gov
/Organism="Homo sapiens"
/db_xref="taxon:9606"
/db_oref="taxon:9606"
/clone="InAGE:2183297"
/clone_lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
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RESULT 5
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Best Local Similarity 90.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                       22 AAACATGACTGGTATGAAGAAT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               790 gtgaggaaccaggatgagaaaggcggctggccgattatggtgacccgtaagttaggggaa 849
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                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                 HCGP http://www.ludwig.org.br/ORESTES.
The FARESP/LICR Human Cancer Genome Pr
Unpublished (1999)
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp,
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aggttgattgcgaaagggaagggcttcctttgacaacattaccatctctaccacagcccac .756
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                                                                                                                                                                                                                                                                                                                                                                                       ctggccgattatggtgacccgtaagttaggggaaggcttcaagtctttagagccagggtg 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARAAGACCATATATTCCTCAATTCAGC-TTAAGGGCAACAGCCCCTTATAAGTTTCT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=PM3-HT0347-091199-001-b10&t3=1999-11-09&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
                                                                                            AA435342 426 bp mRNA 254
vd49909.s1 Knowles Solter mouse 2 cell Mus
                                                         AA435342
                                                                         IMAGE: 803968 5' similar to WP: B0285.5 CE00644 ;, mRNA sequence
house mouse
                                      AA435342.1 GI:2140162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-Torgan: head_neck; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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                                                                                                      musculus cDNA clone
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                                                                                                                                                                                                                                                                                                                          649 aacacaaaagctgtcaagccaacaagaataatgcccaagaaggtggttaggttgattgcg 708
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                                                                                                                                                   769 ttcgctgccagtgactggctggtgaggaaccaggatgagaaaggcggctggccgattatg
                                                                                                                                                                                                                                                                709 aaagggaagggcttccttgacaacattaccatctctaccacagcccacatggctgccttc 768
    302
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                                                                          gtgacccgtaagttaggggaaggcttcaagtctttagagccagggtggtactccgccatg
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
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1 (bases 1 to 426)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Possible reversed clone: similarity on wrong strand Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
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Site_1: Miul; Site_2: Sall; Cloned unidirectionally from
mRNA prepared from 13,500 2-cell stage embryos. Primer:
Sall(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTTTTTTT-3', cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."

97 c 107 g 96 t
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/tissue_type="embryo"
/dev_stage="2-cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="IMAGE:803968"
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Pred. No. 8.2e-97;
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               594 gagcacagttacccgggacctggtcactgacctcaggaaaggagtgggtctttccaacac 653
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65 AAAAGCTGTCAAGCCAACCAAAATCATGCCCAAAAAGGTGGTTAGGTTGATTGCAAAAGG 124
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                                                        GAGTACAGTTACCAGAGAGCTGGTCACTGACCTCAGGAAAGGAGTGGGCCTGTCTAACAC 64
                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Nouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:613262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 455)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vr48g04.s1 Knowles Solter mouse IMAGE:1123926 5', mRNA sequence.
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                                                                                                                                                                                                                   138
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouseest@watson.wustl.edu
                                                                                                                                                                                                     /clone="IMAGE:1123926"
/clone_lib="Knowles Solter mouse 2 cell"
/tissue_type="embryo"
/dev_stage="2-cell"
                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="B6D2 F1/J"
                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
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                                                                                                                               24.7%; Score 346.6; DB 12; Length 455; 88.0%; Pred. No. 1.4e-91;
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AUTHORS
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363 TCAGTCAGCTTTAGGG-----CACAGCCATACAAGTTTCCGTCAGAGCAGCATGGAGTTAA 418
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                                                                                                                                                                                                                                                    Submitted (12-ARR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                      http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F., Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodon nigroviridis DNA sequence
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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/clone_lib="G"
/note="Genoscope sequence ID : COAG200CE12LP1-end :
1 280 c 264 g 158 t
                                                                                                            /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
.clone="200J23"
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                                                                                                                                                                               ACGACCTGCGCCACTTCATG 866
                                      vd49909.xl Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:803968 3' similar to TR:018756 018756 C5-GLUCURONYL EPIMERASE
    AI467374
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                                                                                                                                                                                                642 tetttecaacacaaaagetgteaageeaagaataatgeeeaagaaggtggttaggtt 701
                                                         822 gattatggtgacccgtaagttaggggaaggcttcaagtctttagagccagggtggtactc 881
                                      241 AATTATGGTGACCCGGAAGTTAGGGGAAGGGTTTAAATCTTTAGAACCAGGATGGTACTC
                                                                                                                                           762 tgccttcttcgctgccagtgactggctggtgaggaaccaggatgagaaaggcggctggcc
                                                                                                                                                                                                                                                                               61 CCTTTCTAACACAAAAGCTGTCAAGCCAAACCAAAATCATGCCCAAAAAAGGTGGTTAGGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                    Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Waterston, R. and Wilson, R. The WashU-NCI Mouse EST Project 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI: 480312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 358)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone was previously sequenced on the 5' end only, this new data is from the 3' end % \left( 1\right) =\left( 1\right) ^{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Organ: embryo; Vector: pBluescribe (modified); site_1: MluI; Site_2: SalI; Cloned unidirectionally from SITE_1: MluI; Site_2: SalI; Cloned unidirectionally from Taylor of the MluI; Site_2: CDNAS were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NEB).

Average insert size: 1.2 kb."

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/clone_lib="Knowles Solter mouse 2 cell"
/tissue_type="embryo"
/dev_stage="2-cell"
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                               480 tctggagacgacagaaagaatcagctcttcactgtacattatgtctcaaatacccagct 539
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                                                                                                                                                                                                                                         363 TGTTGGTATATTCTCCCCTACAGGAACCAGTGAAGGTGTATCCTTGCAACTGGGAAACAC 304
                                                                                                                                                                                                                                                                            360 tgttaaacagttcattgctccagaaaccagtgaaggtgtatccttgcaactggggaacac 419
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                                                                                                                    303 AAAAGATTTTATTATTTCATTTGACCTCAAGTTCTTGACAAATGGAAGTGTGTCCGTGGT 244
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   TCTAGAGACCACAGAAAAGAATCAGCTCTTCACTATACATTATGTCTCAAATGCTCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 434.
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300-137-e07&t3=2000-03-16&t4=1)
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Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/clone_lib="HT0539"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single pass sequencing. Bases ov0.980904.e. Vector identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: 40 row: B column: 6
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST discovery in swine
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Fahrenkrug, S.C., Fr
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Sus scrofa
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BF080558.1 GI:10874460
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                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Sus scrofa"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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133 gaaggtgtacctttatctacacagtggggacctcaaggctatttctacccaatccagatt 192
                                                                                                                                                                         73 atgtcctttgaaggctacaatgtggaagtccgagacagagtcaagtgcataagtggggtt 132
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                                                              ATGTCCTTTGAAGGCTACAATGTGGAAGTCCGAGACAGAGTCAAATGCATAAGTGGGGTT 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." 107 c 135 g 142 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Freking, B.A., Rohrer, G.A.,
                                                                                                                                                                                                                                                                                                                             Score 285.4; DB 143; Length 566; Pred. No. 2.1e-73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            496 GTATATGAAACAGCAGAAGACAGGGACAAAAGTAACAAGCTCAGTGACTGGACTGTGCCA 555
                                                                                                                                    119 gcataagtggggttgaaggtgtacctttatctacacagtggggacctcaaggctatttct 178
                                                          61 ATCCCATCCAGATCGCACAGTACGGGTTGAGTCACTACAGCAAAAAACCTGACCGAGAAGC 120
                                                                                                                     1 GCATAAGTGGTGTTGAAGGTGTGCCCTTATCCACCCAGTGGGGACCTCAGGGCTACTTCT 60
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 CCCCGCACATCGAGGTGTACGAAACGGCCGAGGAGAAGGACAGGGGCAGCAGGGCTGCTG
                 cccttatatagaggtatatgaaacagcagaagacagggacaaaaaacagcaagcccaatg 298
                                                                          acccaatccagattgcacagtatgggttaagtcactacagcaagaatctaactgaaaaac 238
                                                                                                                                                                                   352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI981391 590 bp mRNA EST pat.pk0052.c6.f chicken activated T cell cDN clone pat.pk0052.c6.f 5' similar to KIAA0836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tirunagaru, V.G., Sofer, L., Cui, J. and Burnside, J. An expressed sequence tag database of T-cell-enriched activated chicken splenocytes: sequence analysis of 5251 clones Genomics 66 (2), 144-151 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Joan Burnside Molecular Endocrinology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Seg primer: T7
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                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        joan@UDel.Edu
                                                                                                                                                                                                                                                                                                                                                                                                               1. .590
                                                                                                                                                                                                                                                                           /note="Vector: pcDNA3" 165 c 160 g
                                                                                                                                                                                                                                                                                                      /cell_type="Con A-activated splenic T cell"
/lab_host="E.coli TOP10 F'"
                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                 /clone="pat.pk0052.c6.f"
/clone_lib="chicken activated T cell cDNA"
                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:903]
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Gallus gallus"
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                                                                                                                                                                                                                                                                                           collaborative arrangements Seg primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301 443 1706 Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Chin, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97044477
                                                                                                                                                                                                                                                                                                                                                                                                       Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse
       100
                                                                                                                                                                                                                                      /strain="C57BL/6J"
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241 GTGTTAAACACTTTGTTGCTCCAGAGACACCGAGGGGGTTTCCCTGCAGCTTGGCAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; Sciurognathi; 1 (bases 1 to 381)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE861166 381 bp mRNA EST 29-SEP-2000 UI-M-AMO-adu-h-07-0-UI.rl NIH_BMAP_MAM Mus musculus cDNA clone UI-M-AMO-adu-h-07-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, 20892-9643, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            availability will be considered under appropriate and limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: M.B. Soares Lab Clone distribution:
by Bonaldo, Lennon and Soares, Genome Research, 1996. Tissue provided by Ms. Annie Novakovich. Zivic-Miller Laboratories."
                                                                        NIH_BMAP_MAN library is a non-normalized library NIH_BMAP_MAN library is a non-normalized library constructed from mouse amygdala. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
                                                                                                                                                                                                                                     /lab_host="DH10B (Life Technologies)"
/note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The
                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="UI-M-AM0-adu-h-07-0-UI"
/clone_lib="NIH_BMAP_MAM"
/dev_stage="27-32 days"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                 Email: genome-resertc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
'N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
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Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                  ,Y. and Hayashizaki,Y.
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
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1 (bases 1 to 251)
Alzawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Alzawa, K., Akahira, S., Akimura, T., Hirozane, T., Hodoyama, Y., Hiragaki, T., Hayatsu, N., Kawai, J., Kojima, Y., Konno Totani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C., 
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Tel: +81-298-36-901
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Unpublished (2000)
Contact: Yoshihide Hayashizaki
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93.2%;
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                         TITLE
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                                                                                                                                                                                                                                                                                                                                                                241 TGGGGTATATA 251
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                                                                                                                                                                                            AV672171 684 bp mkNA
AV672171 Nori Satoh unpublished cDNA library Ciona
cDNA clone citb2b15 5', mRNA sequence.
                                                                                                                   Ciona intestinalis.
Unpublished (2000)
          Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T. Expressed genes in Ciona intestinalis
                                                                                       Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
                                                                                                                                                                  EST
                                                                        Phlebobranchia; Cionidae; Ciona.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI" 36 c 67 g 77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
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/dev_stage="egg"
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                                                                         604 CCAATTTTTTGATGCAAGCCAATGGATGTATTTAAACCAAGACAAGAAGACTGGAGGGTG 663
                                                                                             762 tgccttcttcgctgccagtgactggctggtgaggaaccaggatgagaaaggcggctggcc 821
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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Department of Zoology
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/clone=lib="Nori Satch unpublished cDNA library"
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/db_xref="taxon:7719"
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Search completed: May 25, 2001, 03:23:20 Job time: 5137 sec

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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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                                                                  Submitted (14-MAY-1997) Medical and Physiological Chemistry, Biomedical Center, Husargatan 3, Uppsala 751 23, Sweden Location/Qualifiers
                                                                                                                                                                                                                  AF003927
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                              Li, J.-P. and Lindahl, U
                                                                                                                    bovine lung
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Submitted (16-FEB-2000) to the DDBJ/EMBL/GenBank databases. Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yan Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952, Pax:81-438-52-3952, Pax:81-438-52-
                                                                                                                                                                                                                                                                                                                                                Isogai.T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuk Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakawa,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatu,A., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatu,A., Nanamoto,J., Wakamatu,A., Nanamoto,J., Wakamatu,A.,
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                                            ATTACCATCTCTACCACAGCCCACATGGCTGCATTTTTTTGCTGCTAGTGATTGGCTAGTA
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/note="cloning vector: pME18SFL3"
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/db_xref="taxon:9606"
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Homo sapiens mRNA for KIAA0836 protein,
AB020643
                                                                                                                                 Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Hirosawa,M., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O. Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro DNA Res. 5 (6), 355-364 (1998)
          Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)
                                                                 Direct Submission Submitted (02-DEC-1998) to the DDBJ/EMBL/GenBank databases. Osamu
                                                                                          Ohara, O., Suyama, M., Kikuno, R., Nagase, T. and Ishikawa, K.
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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INDEHTI KGRREGNEWFLPFTYWYEKYEDYYCKVVQYDGYDREFESHSYSKVYAQRAPY
INDEHTI KGRREGNEWFLPFTYWYEKYEDYYCKVVQYDGYDREFESHSYSKVYAQRAPY
INDEHTI KYEZPAEDRIKKENKOMINTUPKGCFMANVADKSFTINVKQFIAPETSEGVSL
TEKPPHIEVYEZPAEDRIKKENKPHDWTVPKGCFMANVADKSFTINVKQFIAPETSEGVSL
QLGNTKDFII SFDLKFLTNGSVSVVLETTEKNQLFTHYVSNAQLIAPKKENDLYYGIG
PRTSWSTYTRDLYTDLRKGVGLSNTKAVKFTKLMPKKVVLIARGKGFLDNITISTTA
HMAAFFAASDMLVRNQDEKGGWPIMVTRKLGEGFKSLEPGWSAMAQGQAISTLVRAV
LLTKDHIFLNSALRATAPYKFLSEQHGVKAVFMNKHDWYEEYPTTPSSFVLNGFMYSL
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/protein_id="BAA74859.1"
/db_xref="GI:4240161"
/translation="NYKTLIIICALFTLYTYLLWNKCSSDKAIQFPRRSSSGFRVDGF
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/dev_stage="adult"
/sex="male"
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Mammalia; Eutheria; Rodentia; Sciurognati 1 (Dases 1 to 2088)
Crawford, B.E., Olson, S.K., Pinhal, M.A.S.
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Crawford, B.E., Olson, S.K., Pinhal, M.A.S. and Esko, J.D
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of California, San Diego, 9500 Gilman Drive, La Jolla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-DEC-2000) Cellular and Molecular Medicine,
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//translation="MRCLAARVNYKTLIIICALFTLVTVLLMNKCSSDKAIQFPRHLS
//translation="MRCLAARVNYKTLIIICALFTLVTVLLMNKCSSDKAIQFPRHLS
//translation="MRCLAARVNYKTLIIICALFTLVTVLLMNKCSSDKAIQFPRHLS
//translation="MRCLAARVNYKTLIIICALFTLVTVCKVVQKOGFNSNGGSKVLGL
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LSHYSKNLTEKPHIEYYETAEDDRNIRPWFVPKGEFMASVADKSRSTNVKQFIA
PETSEGVSLQLGNTKODFISFVDLKLINGGSVSVVLETTVEKVQLETVHYVSNTQLIAFR
DRDIYYGIGPRTSWSTVTRDLVTDLRKGYGLSNTKAVKFTKINFKKVVRLIAKGKGFL
DNITISTTAHMAAFFAASDMLVRNQDEKGGMFINVTRKLGEGFKSLEPGWYSAMAQGQ
AISTLVRAYLLTKDYVFLSSALRATAPYKFPSEGHGVKAMIDWYEBYPTPSSF
VILNGFWYGTIGTIVTLEFFAGFTTGKEABDT VEFDRAFGIKAMIDWYEBYPTTPSSF
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo, sapiens chromosome 15, clone RP11-352D13
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                                                                                                                                                                                                                                                                                                                                                                                                 * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.w1.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 3.5 in Q20 bases; agarose-fp quality coverage: 3.4 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 163000; agarose-fp Insert size: 164287; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
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                                                                                              2789: contig of 1554 bp in length 2790 2889: gap of 100 bp 2890 4922: contin of 100 bp 4923 contin of 100 bp
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1136 1235: gap of 100 bp
1236 2789: contig of 1777
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                                             3 5022: gap
6180:
                6280:
        contig of 2033 bp in length
of 100 bp
contig of 1158 bp in length
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140028 167187: cont
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12891 15198: contig of 2008 bp in length
15199 15298: gap of 100 bp
15299 17490: contig of 2192 bp in length
17491 17590: gap of 100 bp
17591 20019: contig of 2429 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54850 54949: gap of 100 bp 54950 58121: contig of 3172 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76629 76728: gap of 100 bp 16729 85215: contig of 8487 h
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4033 37691: contig of 3659 bp in length
7692 37791: gap of 100 bp
7792 42856: contig of 5065 bp in length
2857 42956: gap of 100 bp
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9550 11032: contig of 1483 bp in length
103 11132: gap of 100 bp
1133 12790: contig of 1658 bp in length
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9550. .11032
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30782: contig of 3583 bp in length
30882: gap of 100 bp
33932: contig of 3050 bp in length
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95800: contig of 10485 bp in length
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76628: contig of 5748 bp in length
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70780: contig of 6431 bp in length
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49339: contig of 6383 bp in length
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                                                                                                                                                                                                                                                                SEQUENCE,
AC073380
                                                                                                                                                                                                                                                                      HTG 28-JUN-2000 HOMO Sapiens chromosome 17 clone RP11-82G5 map 17, WORKING DRAFT SEQUENCE, 22 unordered pieces.
Anderson, S., Baldwin, J., Barna, N., Boguslavkiy, L., Boukhgalter, B., Bro
                                  Birren, B., Linton, L.,
                                                                                                                Birren, B., Linton, L., Nusbaum, C. and
                                                                       Unpublished
                                                                                           Homo sapiens chromosome
                                                                                                                            Mammalia; Eutheria; Pr
1 (bases 1 to 171073)
                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                               HTG;
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                                                        (bases 1 to 171073)
                                                                                                                                                                                                                           HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                   Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
J., Barna,N., Bastien,V., Beda,F.,
                                                                                           17, clone RP11-82G5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-JUN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jun 28, 2000 this sequence version replaced gi:8567836. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               consists of 22 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; M77815; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 consensus quality: 158402 bases at least 040 consensus quality: 165231 bases at least 020 consensus quality: 167603 bases at least 020 insert size: 168973; sum-of contigs
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Center clone name: 82_G_5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage: 4.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site:
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14454: contig of 1891 bp
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38: gap of 100 bp
6461: contig of 100 bp
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338: gap of 100 bp
19574: contig of 2736 bp in
574: gap of 100 bp
21309: contig of 1635 bp in
109: gap of 100 bp
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51: gap of 100 bp
8310: contig of 1749 bp in length
10: gap of 100 bp
10590: contig of 2180 bp in length
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9: gap of 100 bp
2848: contig of 1389 bp in length
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contig of 2184 bp
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48711 58240: contig of 9530 bp in length
58241 58340: gap of 100 bp
58341 68915: contig of 11575 bp in length
69916 70015: gap of 100 bp
70016 8336: contig of 13321 bp in length
8337 83436: gap of 100 bp
68347 96601: contig of 13165 bp in length
98602 96701: gap of 100 bp
98602 96701: gap of 100 bp
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113777 136870: contig of 23094 bp in length
136871 136970: gap of 100 bp
136971 171073: contig of 34103 bp in length
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96702. .113676
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58341. .69915
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12564, 14454
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/db_xref="taxon:9606"
/chromosome="17"
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17309: gap of 100 bp

34663: contig of 7354 bp in length

14763: gap of 100 bp

41925: contig of 7162 bp in length

12025: gap of 100 bp

48610: contig of 6585 bp in length
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                                                                                                                                                                                                               TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    928 ctcttaacaaaagaccatatattcctcaattcagctttaagggcaacagccccttacaag 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cacaccaccacatcaatcaactgcagctgcttagcaccattgatgagtccccaatcttc 1347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATACCACCCACATCAATCAGTTGCAGCTACTCAGTACCATTGATGAGTCCCCAGTCTTC 4578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTCTATCTGAGCAGCATGGAGTTAAAGCTGTGTTTATGAATAAACATGACTGGTATGAA
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand,Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
                                                      Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boughslavkty,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArtellano,K., Dewar,K., Disz,J.S., Collymore,A., Cooke,P., DeArtellano,K., Dewar,K., Disz,J.S.,
                                                                                                                                                                                    Homo sapiens chromosome 15,
Unpublished
                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 167187)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                   HTG;
                                                                                                                                                                                                                                                                                                                                                                                                        AC026992 167187 bp DNA HTG 03-JUL-2000
Homo sapiens chromosome 15 clone RP11-352D13 map 15, WORKING DRAFT
SEQUENCE, 30 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC026992
                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      AC026992.4 GI:8901256
                                                                                                                                                                                                                                                                                                                                human.
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/note="assembly_fragment"
55739 a 30189 c 29971 g 53068
                                                                                                                                                                 (bases 1 to 167187)
                                                                                                                                                                                                                                                                                                                                                 HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    167187 bp
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                                                                                                                                                                                                       Nusbaum, C. and Lander, E. me 15, clone RP11-352D13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 490.6; DB 75
Pred. No. 1.6e-123;
D; Mismatches 29;
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Howland, J.C.,

Johnson, R.,

Jones, C

Karatas, A.,

JOURNAL

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Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehozky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., OʻConnor, T., OʻDonnell, P.,
OʻNell, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (25-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 3, 2000 this sequence version replaced gi:8079836. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RN/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rarbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 163000; agarose-fp Insert size: 164287; sum-of-contigs Ouality coverage: 3.5 in O20 bases; Ouality coverage: 3.4 in O20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 Consensus quality: 147074 bases at least Q40 Consensus quality: 157353 bases at least Q30 Consensus quality: 161662 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L8712
Center clone name: 352_D_13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seg.wi.mit.edu
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1236 2789:
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100 bp r 11 length
120 20119: gap of 100 bp in length
20 23909: contig of 3790 bp in length
10 24009: gap of 100 bp
0 27099: contig of 3090 bp '-
0 27199: gap of
                                                                                                                                                                                                                                                                                                                                                                                     1 6280: gap o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2889: gap
4922:
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11032: contig of 1483 bp in
11132: gap of 100 bp
                                                                                                                                                             15198: contig of 2308 bp in
15298: gap of 100 bp
17490: contig of 2192 bp in
                                                                                                                                                                                                            12790: contig of 1658 bp in
12890: gap of 100 bp
15198: contig of 2308 bp in
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100 b

100 c

11032; cc
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5: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q20 bases; agarose-fp Q20 bases; sum-of-contigs
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of 1271 bp in length
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1798 bp in length
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2033 bp in length
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114861 114960: gap of 100 bp
114961 123755: contig of 8795 bp in length
123756 123865. am of
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123856 139927: contig of 16072 l
                                                                              vector_side:right"
27200. .30782
                                                                                                                             clone_end:T7
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                     12891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
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                                                                                                                                               /note="assembly_fragment
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95800: contig of 10485 bp in length
95800: gap of 100 bp
105851: contig of 9951 bp in length
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58121: contig of 3172 bp in
58221: gap of 100 bp
64249: contig of 6028 bp in
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49339: contig of 6383 bp in
49439: gap of 100 bp
54849: contig of 5410 bp in
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30882: gap of 100 bp
33932: contig of 3050 bp in length
34032: gap of 100 bp
37691: contig of 3659 bp in length
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76628: contig of 5748 bp in length
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         AUTHORS
TITLE
JOURNAL
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                                           Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 29372)
Direct Submission
Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                             Drosophila melanogaster,
                                                                                                                                      HTG; HTGS_PHASE2
                                                                                                                                                                        AC018117
                                 Adams, M. and Venter, J.C.
                                                                                                                           fruit fly.
                                                                                                                                                     AC018117.1 GI:6553074
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123856. .139927
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76729. .85215
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37792. .42856
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70881. .76628
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                                                                                                                                                                                                              DNA
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RESULT 9
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Best Local Similarity
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          Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.H., Park, S., Pfeiffer, B., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Wabster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M. Sequencing of Drosophila melanogaster
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musconorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACUU/393 11959/ bp DNA HTG 21-FEB-2000
Drosophila melanogaster chromosome 2 clone BACR01C10 (D620) RPCI-9:
01.C.10 map 42E-43A strain y; cn bw sp, *** SEQUENCING IN PROGRESS
*** 80 NOOTAGE 3 income
                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
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This sequence was identified as CDM:10213417 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                       Eukaryota;
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/db_xref="taxon:7227"
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Celniker, S. E., Agbayani, A., Arcaini Butenhoff, C., Champe, M., Chavez, C., Doyle, C.M., Farfan, D. E., Galle, R., Hoskins, R.A., Hummasi Kim, E., Lee, B., Lewis, S., Li, P., Li, Hoskins, R.A., Houston, K.A., Hummasi Kim, E., Lee, B., Lewis, S., Li, P., Li, Hoskins, R.A., Houston, K.A., Hummasi Kim, E., Lee, B., Lewis, S., Li, P., Li, Hoskins, R.A., Houston, J. E., Galle, R., Hoskins, R.A., Houston, J. E., Galle, R., Hoskins, R.A., Moshrefi, M., Nixon, Pfeifffer, B., Poon, L., Sequeira, A., Svirskas, R.R., Wan, K. H., Weinburg, Rubin, G.M.  Direct Submission  Submitted (20-MAY-1999) Drosophila Laboratory, MS 64-121, Berkeley, C. On Feb 21, 2000 this sequence verse For further information about this and relationship to other sequence, archive Web site (http://www.fruit to bdgpefruitfly.berkeley.cdu. All the following cutoffs: length >= 2  * NOTE: This is a 'working draft', * consists of 89 contigs. The true * is not known and their order in * arbitrary. Gaps between the cont * This record will be updated with * as soon as it is available and t * be preserved.  1 584: contig of 584  * 1364 2182 2261: gap of unknow * 1364 2182 2361: gap of unknow * 1364 2362: contig of 596  * 5967 5064: gap of unknow * 1983 10801 1080: gap of unknow * 1985 10801 1080: gap of unknow * 1985 10801 1080: gap of unknow * 1985 10801 1080: gap of unknow * 1980 1080: gap of unknow * 1981 1080: gap of unknow * 1981 1080: gap of unknow * 1080 1080: gap of unknow *	
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Chew, M., Ciesiolk Ceorge, R.A., Marci, I.S.R., Karra, K., motan, M.A., Mazda, M.A., Mazda, M.A., A., Mazda, M.A., A., Mazda, M.A., A., Mazda, M.A., Sethi, H., Snir, E., Zhang, R., Zhera Sethi, H., Snir, E., Zhera Sethi, H., Snir, E., Zhera Sequence, Including replaced gi:488 sequence, Including please visit our replaced gi:488 sequence, Including the finished sequence recorder of the piece order of the piece finis sequence recording are represented the finished sequence represented fine gaps are unknown the finished sequence represented finished sequence represented fine gaps are unknown length be in length l	
Blazej,R.G., a,L., s,N.L., p., p., rk,S., in,L.L. and in,L.L. and sequence or send email bmission meet ttly s a as lown. since will	
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2225; contig of 1277 bp in length 23862; gap of unknown length 25201; contig of 1239 bp in length 25201; contig of 1030 bp in length 26311; contig of 1030 bp in length 26311; contig of 1030 bp in length 26391; gap of unknown length 26391; gap of unknown length 27384; gap of unknown length 2736; contig of 914 bp in length 2736; contig of 914 bp in length 2752; contig of 640 bp in length 2754; contig of 640 bp in length 2754; contig of 1012 bp in length 2754; contig of 1014 bp in length 2754; contig of 1240 bp in length 2757; contig of 1240 bp in length 2757; contig of 1601 bp in length 2757; contig of 1607 bp in length 2755; gap of unknown length 2755; contig of 1750 bp in length 2755; gap of unknown length 2	

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                                          ACU07624 167062 bp DNA HTG : 13-DEC-1999
Drosophila melanogaster chromosome 2 clone BACR10F15 (D621) RPCI-9
10.F.15 map 42E-43A strain y; cn bw sp, *** SEQUENCING IN PROGRESS
AC007624.5 GI:6563437
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                             25 unordered pieces.
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On Dec 13, 1999 this sequence version replaced gi:5670596.
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contlys in this submission meet the following cutoffs: length >= 200 bases.
**NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as truns of N, but the exact sizes of the gaps are unknown.

**This record will be updated with the finished sequence.
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2 (clniker, S.E., Apbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Ffeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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Submitted (21-MAY-1999)
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Drosophila melanogaster genomic scaffold 142000013386042 section of 2, complete sequence.
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
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/strain="y; cn bw sp"
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106831:
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contig of 608 bp in length
gap of unknown length
contig of 695 bp in length.
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contig of 27823 bp in length
gap of unknown length
contig of 23214 bp in length
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MEDLINE
REFERENCE
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TITLE
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Miklos, G.L., Abril, J.F., Agbayani, A., An, H.J.,
Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A.,
Baxendale, J., Bayraktaroglu, L., Beasley, E.M., Besson, K.Y.,
Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D.,
Benos, P.V., Berman, B.P., Bhandari, P., Brottier, P., Burtis, K.C.,
Busam, D.A., Butler, H., Cadieu, E., Center, A., Chandrai,
Busam, D.A., Butler, H., Cadieu, E., Center, A., Chandrai,
Busam, D.A., Butler, H., Cadieu, E., Center, A., Chandrai,
Busam, D.A., Butler, H., Deng, Z., Mays, A.D., Dew, I., Davies, P., de
Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M.,
Dodson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dunkov, B.C.,
Dunn, P., Durbin, K.J., Evangelista, C.C., Ferraz, C., Ferriera, S.,
Fleischmann, W., Fosler, C., Gabrielian, A.E., Garg, N.S.,
Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z.,
Guan, P., Harris, M., Harris, N.L., Harvey, D., Heiman, T.J.,
Guan, P., Harris, M., Kalush, F., Karpen, G.H., Ke, Z.,
Wei, M.H., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z.,
Kenison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C.,
Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A.,
Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A.,
McLeod, M.P., McSheelson, D., Merkulov, G., Milshina, N.V., Mobarry, C.,
Morris, J., Moshrefi, A., Mount, S.M., Murphy, B., Murphy, L.,
Muzny, D.M., Nelson, D.L., Nelson, K.A., Nixon, K.,
Sanders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I.,
Sanders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Klamos,I., Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C., Stapleton,M., Strong,R., Sun,E., Svirskas,R., Tector,C., Turner,R., Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A., Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A., Weissenbach,J., Williams,S.M., Woodage,T., Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F., Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H., Zhong,F.N., Zhong,W., Zhou,S., Zhu,S., Smith,H.O., Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster Science 287 (5461), 2185-2195 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfelffer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, K.H., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, Man, K.H., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Man, M.H., Gabor Man, M.H., Man, M.H., Man, M.H., Man, M.H., Man, M.H., M
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AE003789.2 GI:107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J. Direct Submission Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Oct 9, 2000 this sequence version replaced g1:7302263 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rockville, MD, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 299474)
                                                                                                              /db_xref="FLYBASE: FBgn0010347"
<11901. .>38332
/gene="1.28"
                                                                                                                                                                                                                                                                                                             from the published sequence for this transcript/product="CT9093"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(11901. .12167,12272. .12335,12376. .13327,37670. .38167,
38362. .38332)
/gene="1.28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .299474
                              /map="42A13-42A16"
                                                                      /note="CG9397"
                                                                                                                                                                                                                                                                /db_xref="FLYBASE:FBan0009397"
                                                                                                                                                                                                                                                                                                                                                                                              /note="Nucleotide sequence of the Celera sequence differs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:10727129
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                                                                                      /db_xref="FLYBASE:FBan0009403"
/db_xref="FLYBASE:FBgn0033077"
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                                                                                                                                                                                                                   /db_xref="FLYBASE:FBgn0040673"
/evidence=not_experimental
/protein_id="AptS7357.1"
/db_xref="GI:7302266"
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WPRVKEGGGGCLSPAAIDRVEQIEKQQKKSA"
join(123398. 1123479,123714. 112350,125546. 1127154,
127220. 1127811,127850. 112797,128173. 1128350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
complement(116891..117118)
/gene="CG15234"
                                               /gene="CG9403"
/man="/
                /db_xref="FLYBASE:FBan0009403"
                                           /map="42B2-42B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental complement(<116891, .>117118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(<116891.
/gene="CG15234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTESIYLTQKVWAGCALGPGKGLEPRVGRRHGHNAIVIVAMEKSSPPPQE"
complement(<116891. .>117118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSSGALNTLAIVLLLMPGAYVHQWVVPEEDYHSDLKGYIETFCC
LYSPSIGCQLALNPGIFNKEKLPVRRCKDCIEHCQCSNKSTPPLKPRMVVSLLGMFAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSQLYQGARKTATTSRVGVGKTTTVATAPRTTGGERGTKGSKKRCLDRYDSSESSDR*complement(join(<109514. 109577,109653. 109695,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="CG15234 gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="FLYBASE:FBan0015234"
/db_xref="FLYBASE:FBgn0040673"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="FLYBASE:FBan0015233"
/db_xref="FLYBASE:FBgn0033076"
/protein_id="AaF57356.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="FLYBASE:FBan0015233"
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complement(join(109514. .109577,109653. .109695,
109991. .110233,110341. .110397,110536. .110587))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(<109514.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="msvTQPKDTALKTKESAAEVAAPLAPLSVKTAGATGRKTLTSSA
ALSUFDQLKNSVNTNSLTIGAGVGNNSSPEATPPITAPASTTTASPILTPKSPPPTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="FLYBASE:FBgn0010347"
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/db_xref="GI:7302264"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
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/db_xref="FLYBASE:FBgn0033076"
complement(<109514 ...>110587)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="CG15234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'db_xref="FLYBASE:FBan0015234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product="CT35171"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="FLYBASE:FBgn0040673"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="CG15233 gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="CG15233"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              map="42B1-42B2"
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/db_xref="FLYBASE:FBgn0010347"
                                                                                                                                                                                                    .>128862)
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G15233"
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Best Local Similarity
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1275 ccgctgggactatcacaccaccacatcaatcaactgcagctgcttagcaccattgatga 1334
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Db 180165 TGGAAAGCTTTTCGCGCAGGGCATGCACTCCCTTAAAAAGATGCTGTTGCTATTTGACAC 180106
                                                                                                                                                                                                                                                                                                                                                                                                                       Db 180285 TTACAGGTACGAGGAGTACCCCACCACGCCACCCTCTTATGTGCTAAACGGCTTTATCTA 180226
                                                                                                                                                                                                                                                                                                                       1095 ttctttaattgggctgtatgacttaaaagaaactgcaggggaaaaattggggaaagaagc 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1035 tgactggtatgaagaatatccaactacacctagctcttttgttttaaatggctttatgta 1094
                                     tggctcaggaaccatctatgacctccggcacttcatgcttggcattgcccccaacctggc 1274
                                                                                                                                                                                                                                                                              TTCACTGCTGGGTCTCTACGATCTCAACAGCACTGCCCCGGGAAAAATCGCCCGGGAGGC 180166
TGGCTCCGGCACCAGCTACGACCTGCGCCCATCTGAGCCTGGGCGTAGCTCCTAATCTGGC 180046
                                                                                                                                                                                                       gaggtccttgtatgagcgtggcatggaatcccttaaagccatgctccccttgtacgacac 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="FLYBASE:FBan0003161"
/db_xref="FLYBASE:FBgn0004145"
complement(join(136536. 137283,137341. 137530,
141637. 141750,142605. .142690))
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/db_xref="FLYBASE:FBgn0004145"
complement(join(136536. .137283,137341.
141637. .141750,141934. .142026))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPQRAJVKPPLHSSTQPPPLYTISSMEACSPAAASSPAAKRSLPAAKPYQKRLTAKGR
VGTAPIIATPTTPPPLVPTSATKELGQLRKSTGTGTGTPPTGTPTPPLVSIAPSKLTP
TLSVSKQGPTMKLANSAPDLFDLVKNSKLVAKVSQPLTPLPESSPSSSSMSGKGKGK
RSSPALSTSNSCTLSAFSKIKVETTELASQTGSLTSSSIPTISLKPQSFAGQLPKREP
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SNSCOMMFVAPLNNQQVGLKDNKLYIVNSAEYLGYLMSLQIALNNQQHQQQQIISAT
QPPPLAATNNNSTNTATQPPPLAATNNTNSNTANNSTASNSININASNNLSNINNTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="Vha16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(136536. .137283,137341.
141637. .141979))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGYCYWDKCNKKHESNSKLLDHMQTHHVNTQTGPFACLWVGCKVYNKESCSRRWLERH
VLSHGGSKQFKCIVEGCGLRFGSQLALQKHVNNHFNATDNARESTSKRTSDPPVPKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SESSNSIADAISSKSASVGPPTTAASSASSSASDSNSLASNAPSPASPEDCSAAPSPA
CSASTIGSIPPSTVUDIAMVEATSKSLPKSAISPILSQPKTIRFPAGAGASGKGGKRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLGSPSPAASNLSASSRRAASQTDMLSELVTSSCISSGGDDCSQATDSPPMPALPLAK
SEDATTPISTVSGGSSSGSSNYDEEDDKSVASLETHQTHKRLRDLPTPESGIGGSLSN
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SGEGSCLTGGGAASAKKARSDLPGSFDASKRLKVAAMEESQTKITGFFKSQMKPSPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"CT40117"
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join(123838. .125350,125546. .127154,127220. .127781,
127850____127997,128173. .128350,128412. .128862)
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/db_xref="GI:7302267"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MPPHILGSASGSSSTAAASPPTSSASQTPPSPAIHHSHLSQHN#/
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63.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 150.8; DB 4
Pred. No. 2.7e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 299474;
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
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CEB0285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                           FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179925 CAAGCACAAC 179916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1395 aaagcacaac 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1335 gtccccaatcttcaaagaatttgtcaagaggtggaagagctaccttaaaggcagccgggc 1394
                              gene
                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-JUN-1994) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: Jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortiun Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; Aminopeptidase; CDC2-like protein kinase; Choline kinase; Glycine-rich domain; Mucin; transfer RNA; tRNA-Leu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone B0285. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erratum:[[published errata appear in Science 1999 Jan
1;283(5398):35 and 1999 Mar 26;283(5410):2103 and 1999 Sep
3;285(5433):1493]]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEB0285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z34533.1 GI:506879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans cosmid B0285, complete sequence.
                                                                                                                                                                                                                                                                                                                    Predicted proteins B0285.8, B0285.9 and B0285.10 are 60-70% identical at the amino acid level. For a graphical representation of this sequence and its analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neighbouring submissions.
The true left end of clone B0285 is at 25507 in sequence AL024499.
The start of this sequence (1. .104) overlaps with the end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Current sequence finishing criteria for the C. elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sulston, J.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The C.elegans Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence ALO24499.
The end of this sequence (41294. .41397) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 available information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 230973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 41397)
                                                                                                                                                                                                                                                                                               http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                       dl] Merged B0285.1 and B0285.2 based on EST data
join(2715. 2908,3445. 3642,5546. 5672,6107. 6220,6278. 6498,6852. 6997,7050. 7339,7398. 7471,7733.
                                                          /chromosome="III"
/clone="B0285"
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                                                                                                                     /db_xref="taxon:6239"
                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 to 41397)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41397 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing Consortium
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/Translation="MELSGGSSTHERDOKGSYGHRERTRSHSGSPSRFYSKDKRGSSR
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RSRHRSPKRSGSSKKSKRRNSKRSSSDLMDTSLMSELKKHODYGSSSKSKKKSKRKR
KHSSSSSSSGEAMDLPVSSNGKNVTALFPPSFNINPFQPMFSQPPPPLPPNSQPM
TPPPRPPAPFSYDIHFAATASFSLSSIPPPSTDIGGASSKRQDPLPMPPD
SKRIATRPYITTRRGHATNRPSDSDSWYKTNLTHYTMLDOJGEGTYGQVYXAVNNUT
EQVALKEVPLENEKEGFPITAIREIKILRQLHHRNIVELMDIVIDISMDELKRTRAN
TYLVERYUDHDLIGLLESKELVDPNKDOJCSLFKOLLEGLAVLHTGFLHRDIKCSNI
LVNNKGELKIADLGLARLMEKESRLYTNRVITTUMYRPELLLGDERKGPADLWSTGC
MLGELFTRKPLFKGNNEEGQLELISKCGSPNVDNWPELTELVGWNTFRMKRTYQRRI
REFFEHLMPREAVDLLDKMLTLMPEKAISAKEALNHWIRSLEHTVOPLKLEOHDOC
REFFEHLMPREAVDLLDKMLTLMPEKAISAKEALNHWIRSLEHTVOPLKLEOHDOC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(2715. .2908,3445. .3642,5546. .5672,6107. .6220, 6278. .6498,6852. .6997,7050. .7339,7398. .7471,7733. 8139. .8333,8382. .8532,8827. .9015)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8139. .8333,8382. .8532,8827. .9015)
/gene="B0285.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"cDNA EST yk173g10.5 comes from this cDNA EST yk173g10.3 comes from this gene cDNA EST yk217f7.3 comes from this gene cDNA EST yk217f7.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JULII(14/79...12919,12968...13145,13248...1
13901...14107,14164...14250,14306...14390)
/gene="80285.4"
                                                                                                                                          Join(14571. .14615,14657. .14818,15191. .15485,15715.
15860. .16018,16144. .16259,16388. .16658,17070. .1721
17776. .18311)
                                                                                                                                                                                                                                                                                        STALLKQIVSQFKQPAFVNYEQFRTSDAFTKVMEQNLGDRGIQLHGLEMCESAEKQEE RFRNAGFKEVKVMDMQIFNNFLDQKEVSRTREIEMLDEMELQQEAHYCVVSARI" JOHN (1457). .14615,14657. .14818,15191. .15485,15715. .158115860. .16018,61144. .16259,16388. .16658,17070. .17288,17776. .183112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA EST yk530f5.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(11398. .11451,11504. .11608,12102. .12397,
12467. .12512))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA84295.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SWISS-PROT:P46553"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="B0285.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="B0285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEMWSKKQKKSARLGRQAEGSSGSGHSIRATSHPRGKAGDELEEIKISDFIFQFSENK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="B0285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3RGGGGGGNKNFGPIDANKCIIPSMWNNPWDALEKEYEQEYGVAITEKVTDPSPSPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA84296.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="contains glycine-rich domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 )AVVSHHADLHAGNYHLIGADLRQANELDQKLATCOLSHDIPTIFIAECVLVYMSADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(12779.
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/protein_id="CAA84297.1"
                                                                         note="cDNA EST yk96a2.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=:
                                                                                                                   'gene="B0285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2779. .12919,12968. .13145,13248. .1
.14107,14164. .14250,14306. .14390)
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                                                                                comes from this gene'
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Query Match
Best Local Similarity
     Conservative
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32550. .32792,32888. .33229,33357. .33515,33765. .33911)
/gene="B0285.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to C. elegans R107.1, K08E5.2; localised similarity to yeast URF YCR37C and rat mucin (PIR:S26784), contains similarity to Pfam domain: pF00939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of similarity with aminopeptidases, contains similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MPFESTEGKCAFVILTMSCYWVAEVVPLAVTSFIPMIALPFLGI
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ITSFISLWISDTACCALMAPIAYALLEEIMIPKMRPBEKENEIEVMKIFDKEDPEEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(21833. .21850,22021. .22170,22213. .22328,22611. .2
22695. .22853,22902. .22945,22990. .23098,23150. .23377,
23585. .23781,23825. .23946,23993. .24295,25051. .25206)
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TPGSFYLNGFLYSLIGLYDLSQLELMIDENDETMRAKIQEAQELYSAGVRSLKQLLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVGAHPLYFSIPTAIGPSFSFMLPMATPANAIVYETKTIRMIDMVSCGVFLNIFCIAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVSGLSSLIACSLNSTISKMPFFVMQIILSIVVVVMTEFSTNSATASIFIPISFKMAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GISYLSWMAFAIPPMIFYMFSSWFIVQLQFLGPRHLMGMFREPTETEKQEEEVAKRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Sodium:sulfate symporter transmembrane region),
Score=153.0, E-value=2.4e-43, N=2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GELTVKQKITQRREQHSHAFYAAADWLVKNQNDRGGWSVPVERSIAERKLVLPPGWHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WKPYEANSSFTVLAKMKQDDLLVLINYVYSEGNGKCVWQEEERISDDYIVQKPKKDGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RCVSAKTDVPMSTQMDPIPYYYPIQISQYGLQHYSRMKLDSISNKSEASPKDDVILGV
NSKEWKGAAGMHETTERLFFNDEQMGKVVNISAGAALANAGAYVYLDKSPDLHVISFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVSYLKKRFDMTGKLGKDGSTFELYTSYAKMRSPDSTYDPLGPFGHFSTYSVETRDRV
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LTQEESRIDEEDEELTQVDVNEDDKKIECEPPGSIESKCIADNGKSMKCWKDEEDVYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLLFIWPKKKPDFRIFRKDKSRPSVRQEPLIDWDCVRRRFPWSIILLLGAGFAISDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WKSYDQLGPMTWAEKSTLVIFVLAVLSWVSSDPKVIPGWSDLFRKGYVTDSCSGLVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKKLDTSRLSVRDRGICKCMMLLVAHASLIGGTGTINSTGPNLIFRDNIEKNFPNEDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAA84299.1"
/db_xref="GI:3873730"
/db_xref="SWISS-PROT:P46556"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(21833...21850,22021...22170,22213...22328,22611...22646,
22695...22853,22902...22945,22990...23098,23150...23377,
23585...23781,23825...23946,23993...24295,25051...25206)
/gene="B0285.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDTGSGTIYDLRHVALGTAPNLARWDYHAVHVYLLKWIAGIEKDEVLSKTADRWIGYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSYSYSYIGNSPIGEWSTVTRDLLVDVARALSSGDNRKKDDNVVLHAGDLRLVSLGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="threonine-rich domain at N terminus; short region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="B0285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(26002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GI:3873728"
/db_xref="SWISS-PROT:P46555"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=
                         5.4%;
                                                                                                                                                                                                                                                                      N EST yk485a8.
N EST yk485a8.
N EST yk327e7.
N EST yk327e7.
                                                                                                                                                                                       EST yk345a2.3 comes
EST yk345a2.5 comes
EST yk266f2.3 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                           lue=1.6e-05, N=1
EST CmM442 comes from this gene
EST EMBL:T02449 comes from this gene
EST EMBL:T00914 comes from this gene
EST EMBL:T02161 comes from this gene
                                                                                                                                                                                                                                                                                                                                                        EST yk51d6.5 comes from this gene
EST yk51d6.3 comes from this gene
EST EMBL:M75802 comes from this gene
EST yk485a8.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        002. .26439,27474. .27738,30045. .30685,31287. .3
.32792,32888. .33229,33357. .33515,33765. .33911)
                                                                                                                                    yk246f6.3 comes
yk246f6.5 comes
     0,
                                                Score 75.8;
                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF01433 (Peptidase family M1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E-value=2.4e-43, N=2"
                                                                                                                                                                                                                                                                         7.3 comes
7.5 comes
     Mismatches
                                                                                                                                                                                                                                                                                                                                                     5802 comes from this gene
                                                                                                                                                                                                                                                                                                                      .5 comes
                                                                                                                 comes
                         8; DB 5;
9.9e-10;
                                                                                                                                 s from this gene
                                                                                                        this gene
                                                     Length 41397;
     Indels
27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score=-130.2,
Gaps
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18269 ATGGATTGGATACGCGTATGGAAAACGGGCAAAACATAA 18307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1365 gtggaagagctaccttaaaggcagccgggcaaagcacaa 1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1305 tcaactgcagctgcttagcaccattgatgagtccccaatcttcaaagaatttgtcaagag 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1032 acatgactggtatgaagaatatccaactacacctagctcttttgttttaaatggctttat 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1092 gtattctttaattgggctgtatgacttaaaagaaactgcaggggaaaaactcggga---- 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTATTGAAATGGATTGCTGGAATTGAAAAAGATGAAGTTTTGAGTAAAACAGCAGATCG 18268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTTGCTTTGGGAACTGCACCGAATCTTGCAAGATGGGATTATCATGCTGTACATGTGTA 18208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cttcatgcttggcattgcccccaacctggcccgctgggactatcacaccaccaccaccatcaa 1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----aagaagcgaggtccttgtatgagcgtggcatggaatc 1184
                                                                                                                                                                                                                        Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 147428 bases at least Q40
Consensus quality: 150614 bases at least Q30
Consensus quality: 15262 bases at least Q20
Consensus quality: 15262 bases at least Q20
Insert size: 15475; sum-of-contigs
Insert size: 15475; sum-of-contigs
Insert size: 151975; 13.3% error; agarose-fp
Quality coverage: 3.45% in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Aug 21, 2000 this sequence version replaced gi:9187197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-JAN-2001) Sanger Centre, Hinxton; Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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PROGRESS *** 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: bA234F20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                   coverage; 3.61x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL160170.4 GI:9863586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROGRESS ***,
NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 156257)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *** SEQUENCING
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Be
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142181 146194; contly of 4014 bp
146195 146294; gap of 100 bp
146295 148386; contly of 2092 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      soon as it is available and the accession number will preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .29457 129556: gap of .29557 131856: cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment:01136
fragment_chain:1"
8945. .26698
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5 8944: gap of 100 bp
5 26698: contig of 17754 bp in length
9 26798: gap of 100 bp
1 50840: contig of 24042 bp in length
50940: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/note="assembly_fragment:00249
                                                                          note-"assembly_fragment:01019
                                                                                                                   note="assembly_fragment:00596"
                                                                                                                                                                                   /note="assembly_fragment:00425"
102652. .113047
                                                                                                                                                                                                                                             /note="assembly_fragment:00554
fragment_chain:3"
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fragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment_chain:1"
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fragment_chain:1"
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/clone_lib="RPCI-11.1"
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                                    note-"assembly_fragment:01103"
                                                                                                                                                         'note="assembly_fragment:00508"
                                                                                                                                                                                                                                                                                                           'note="assembly_fragment:00266
:ragment_chain:3"
                                                                                                                                                                                                                                                                                                                                                                         ragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                          note="assembly_fragment:00274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="assembly_fragment:00186"
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156257: cont
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113047: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53214: gap of 100 bp
64925: contig of 11711 bp in length
65025: gap of 100 bp
102551: contig of 37526 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53114: contig of 2174
53214: gap of 100 by
64925: contig of 1171:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113147: gap of 
126763: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5035: gap of
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4935: (
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129456: contig of 2593 bp
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contig of 10396 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   898 caagccatttctacattagtcagggcctatctcttaacaaaagaccatatattcctcaat 957
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122; Conserv
                                                       only a small overlap as described above.

only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known such as compressions and repeats, but not necessarily within known such as compressions and repeats, but not necessarily within known such as compressions and repeats.
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AL158841
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Human DNA
                                                                                                                                                         on Nov 10, 2000 this sequence version replaced gi:11121381. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                      annotated human repeat sequence elements (e.g. {\rm Alu}). sequence is ambiguous, there is an annotation using
                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (07-NOV-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquirles: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 167721)
The following abbreviations are used to associate primary accession
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fragment_chain:4"
146295. 148386
/note="assembly_fragment:00059
fragment_chain:4"
148487. 156257
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142181. .146194
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fragment_chain:4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/HGP/Chr1
http://www.sanger.ac.uk/HGP/Chr1
RP11-183Ml3 is from the library RPCI-11.1 constructed Roswell Park Cancer Institute by the group of Pieter of further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the entire insert of clone RP11-183M13 The true left end of clone RP5-831021 is at 111240 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECTOR:
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/note="THEIA-internal repeat: matches 1.
                                                                    'note="THEIC repeat: matches 1. .371 of consensus"
                                                                                                                           note="L2 repeat: matches 2627. .2746 of consensus"
                                                                                                                                                       note="Tigger2a repeat: matches 289. .434 of consensus"
6263. .16372
                                                                                                                                                                                                                                 'note="THE1A repeat: matches 1. .354 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MER58B repeat: matches 187. .341 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="MLT11 repeat: matches 41. .410 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MLT1B repeat: matches 212. .389 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1M2 repeat: matches 5168. .5617 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MLT1B repeat: matches 1. .223 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="L2 repeat: matches 2017. .2195 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .16772
                                                                                                                                                                                                                                                                                                                                                  re="THE1A repeat: matches 1. .354 of consensus"
l4. .14507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e-"L1 repeat: matches 4570. .5321 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                              "Tigger2a repeat: matches 1. .289 of consensus"
. .12913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIR repeat: matches 60. .262 of consensus"
                                                                                                                                                                                                              .15021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        .12562
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  'note="L1MC4 repeat:
                              note="L1MC4 repeat: matches 7168. .7388 of consensus"
7634. .58012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20023. .20996
                                                                                              note="L1MA8 repeat: matches 5975. .6291 of consensus"
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                                                                                                                                                                                                  note="MIR repeat: matches 8. .197 of consensus"
                                                                                                                                                                                                                                                                                                 note="MIR repeat: matches 50. .140 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                              note="L2 repeat: matches 2687. .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L1M4 repeat: matches 3246. .3378 of consensus" 9833. .39898
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                                                                                                                                               note="L1PA7 repeat: matches 4863. .6139 of consensus"
                                                                                                                                                                                                                                                 note="L2 repeat: matches 445. .881 of consensus"
                                                                                                                                                                                                                                                                                                                                                    note="MIR repeat: matches 22.
                                                                                                                                                                                                                                                                                                                                                                                                                               2088. .52150
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9667. .49757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MER4D repeat: matches 396. .950 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="MER4D repeat: matches 1. .251 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1M4 repeat: matches 3035. .3259 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="52 copies 2 mer at 63% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="L1M2 repeat: matches 5063. .5678 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L1M4 repeat: matches 2636. .3033 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MERVL repeat: matches 2266. .2621 of consensus"
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9249. .35342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="L2 repeat: matches 2627. .2710 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 e="127 copies 2 mer tt 56% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e="L1M4 repeat: matches 5557. .5647 of consensus"
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                                                                                                                                                                                                                               54826
matches 6605. .7008 of consensus
                                                                                                                                                                                                                                                                                                                                                    .188 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTTTATAGTGTTAACAGCTCTTATGTACAGACAACAGAATCACTAATAATTATTTTCTT 120006
                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 14 clone R-799P8, PROGRESS ***, in ordered pieces. AL136039
                  Center: Genoscope / Centre National de Sequencage Center code: GS
                                                                         Submitted (07-DEC-2000) Genoscope - Centre National de Sequencage BP 191 99106 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
On Dec 9, 2000 this sequence version replaced gi:7708224.
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 174788)
                                                                                                                                                                                                                                                                                                    AL136039.3 GI:11611146
HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                             Direct Submission
Web site: http://www.genoscope.cns.fr/
                                                                                                                                                                                                                                                              Homo sapiens
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67234. .67320
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61921. .61984
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59926. .60232
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50749. .60874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MER5A repeat: matches 7. .131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="MIR repeat: matches 12. .255 of consensus"
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*** SEQUENCING IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                          ORIGIN
                                                                                                                                          BASE COUNT
                       Matches
                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                        STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
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LOCUS

COMMENT

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Mismatches

TITLE

SOURCE

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IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in programd the release of this data is based on the understanding that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vect phage, etc. . . even if efforts are made to eliminate these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percentage of bases with a quality value >= 40 : 99
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Overall quality chart :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from the T7 to the SP6 end.
Upstream BAC (overlapping t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contaminating sequences.
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by the finished sequence as soon as it is available and the accession number will be preserved.

Location/Qualifiers
                                                                                                 53409
Conservative
                                                                                                 ρ
                                                                                            Identified using 34948 c 35572
                                                                                                                                                                                                                                                                                                                                                                                     50407.
                                                                                                                                                                                                                                                                                                                                                                                                                  dbsrs:srs45968
                                                                                                                                                                                                                                                                                                                                                                                                                                     RHdb: RH66038
                                                                                                                                   dbsts:sts28412
                                                                                                                                                                 RHdb: RH97871
                                                                                                                                                                                                                                   dbSTS:STS67895
                                                                                                                                                                                                                                                   RHdb:RH94904
                                                                                                                                                                                                                                                                  RHdb:RH101408
                                                                                                                                                                                                                                                                                                                                 dbSTS:STS45979
                                                                                                                                                                                                                                                                                                                                                      RHdb:RH66049
                                                                                                                                                                               /note="matching EMBL: Z52777
                                                                                                                                                                                                    158308.
                                                                                                                                                                                                                                                                                                                                                                                                 Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                Identified using the e-PCR software (G. 158308. 158439
                                                                                                                                                                                                                                                                                note="matching EMBL:G41930
                                                                                                                                                                                                                                                                                                                 Identified using the e-PCR software
                                                                                                                                                                                                                                                                                                                                                                  /note="matching EMBL:W84782
                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="matching EMBL:T95294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="R-799P8"
               3.0%;
57.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14516
38520
97946
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105
105
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4248
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9727
8979
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               Score 41.6;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The following BAC sequence is oriented
                                                                                               the e-PCR software (G. Schuler) g 50858 t 1 others
                                  DB 83;
   54;
                                Length 174788;
   Indels
                                                                                                                                                                                                                                                                                                                     (G. Schuler)"
                                                                                                                                                                                                                     Schuler)"
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   Gaps
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Qy 292 cccaatga 299
Db 172601 CTGGATCA 172594

Search completed: May 25, 2001, 04:08:32 Job time: 6453 sec

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